

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant	:	Eaton, et al.
Appl. No.	:	10/063,557
Filed	:	May 2, 2002
For	:	SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
Examiner	:	David J. Blanchard
Group Art Unit	:	1642

DECLARATION OF J. CHRISTOPHER GRIMALDI, UNDER 37 CFR §1.132

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

I, J. Christopher Grimaldi, declare and state as follows:

1. I am a Senior Research Associate in the Molecular Biology Department of Genentech, Inc., South San Francisco, CA 94080.
2. My scientific Curriculum Vitae, including my list of publications, is attached to and forms part of this Declaration (Exhibit A).
3. I joined Genentech in January of 1999. From 1999 to 2003, I directed the Cloning Laboratory in the Molecular Biology Department. During this time I directed or performed numerous molecular biology techniques including semi-quantitative Polymerase Chain Reaction (PCR) analyses. I am currently involved, among other projects, in the isolation of genes coding for membrane associated proteins which can be used as targets for antibody therapeutics against cancer. In connection with the above-identified patent application, I personally performed or directed the semi-quantitative PCR gene expression analyses in the assay entitled "Tumor Versus Normal Differential Tissue Expression Distribution," which is described in EXAMPLE 18 in the specification. These studies were used to identify differences in gene expression between tumor tissue and their normal counterparts.
4. EXAMPLE 18 reports the results of the PCR analyses conducted as part of the investigating of several newly discovered DNA sequences. This process included developing

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primers and analyzing expression of the DNA sequences of interest in normal and tumor tissues. The analyses were designed to determine whether a difference exists between gene expression in normal tissues as compared to tumor in the same tissue type.

5. The DNA libraries used in the gene expression studies were made from pooled samples of normal and of tumor tissues. Data from pooled samples is more likely to be accurate than data obtained from a sample from a single individual. That is, the detection of variations in gene expression is likely to represent a more generally relevant condition when pooled samples from normal tissues are compared with pooled samples from tumors in the same tissue type.

6. In differential gene expression studies, one looks for genes whose expression levels differ significantly under different conditions, for example, in normal versus diseased tissue. Thus, I conducted a semi-quantitative analysis of the expression of the DNA sequences of interest in normal versus tumor tissues. Expression levels were graded according to a scale of +, -, and +/- to indicate the amount of the specific signal detected. Using the widely accepted technique of PCR, it was determined whether the polynucleotides tested were more highly expressed, less expressed, or whether expression remained the same in tumor tissue as compared to its normal counterpart. Because this technique relies on the visual detection of ethidium bromide staining of PCR products on agarose gels, it is reasonable to assume that any detectable differences seen between two samples will represent at least a two fold difference in cDNA.

7. The results of the gene expression studies indicate that the genes of interest can be used to differentiate tumor from normal. The precise levels of gene expression are irrelevant; what matters is that there is a relative difference in expression between normal tissue and tumor tissue. The precise type of tumor is also irrelevant; again, the assay was designed to indicate whether a difference exists between normal tissue and tumor tissue of the same type. If a difference is detected, this indicates that the gene and its corresponding polypeptide and antibodies against the polypeptide are useful for diagnostic purposes, to screen samples to differentiate between normal and tumor. Additional studies can then be conducted if further information is desired.

8. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

By: _____

J Christopher Grimaldi

Date: _____

8/10/2004

J. Christopher Grimaldi

1434-36th Ave.
San Francisco, CA 94122
(415) 681-1639 (Home)

EDUCATION

University of California, Berkeley
Bachelor of Arts in Molecular Biology, 1984

EMPLOYMENT EXPERIENCE

SRA

Genentech Inc., South San Francisco; 1/99 to present

Previously, was responsible to direct and manage the Cloning Lab. - Currently focused on isolating cancer specific genes for the Tumor Antigen (TAP), and Secreted Tumor Protein (STOP) projects for the Oncology Department as well as Immunologically relevant genes for the Immunology Department. Directed a lab of 6 scientists focused on a company-wide team effort to identify and isolate secreted proteins for potential therapeutic use (SPDI). For the SPDI project my duties were, among other things, the critically important coordination of the cloning of thousands of putative genes, by developing a smooth process of communication between the Bioinformatics, Cloning, Sequencing, and Legal teams. Collaborated with several groups to discover novel genes through the Curagen project, a unique differential display methodology. Interacted extensively with the Legal team providing essential data needed for filing patents on novel genes discovered through the SPDI, TAP and Curagen projects. My group has developed, implemented and patented high throughput cloning methodologies that have proven to be essential for the isolation of hundreds of novel genes for the SPDI, TAP and Curagen projects as well as dozens of other smaller projects.

Scientist

DNAX Research Institute, Palo Alto; 9/91 to 1/99

Involved in multiple projects aimed at understanding novel genes discovered through bioinformatics studies and functional assays. Developed and patented a method for the specific depletion of eosinophils in vivo using monoclonal antibodies. Developed and implemented essential technical methodologies and provided strategic direction in the areas of expression, cloning, protein purification, general molecular biology, and monoclonal antibody production. Trained and supervised numerous technical staff.

Facilities

Manager

Corixa, Redwood City; 5/89 - 7/91.

Directed plant-related activities, which included expansion planning, maintenance, safety, purchasing, inventory control, shipping and receiving, and laboratory management. Designed and implemented the safety program. Also served as liaison to regulatory agencies at the local, state and federal level. Was in charge of property leases, leasehold improvements, etc. Negotiated vendor contracts and directed the purchasing department. Trained and supervised personnel to carry out the above-mentioned duties.

SRA

University of California, San Francisco
Cancer Research Institute; 2/87-4/89.

Was responsible for numerous cloning projects including: studies of somatic hypermutation, studies of AIDS-associated lymphomas, and cloning of t(5;14), t(11;14), and t(8;14) translocations. Focused on the activation of hemopoietic growth factors involved in the t(5;14) translocation in leukemia patients..

Research
Technician

Berlex Biosciences, South San Francisco; 7/85-2/87.

Worked on a subunit porcine vaccine directed against *Mycoplasma hyopneumoniae*. Was responsible for generating genomic libraries, screening with degenerate oligonucleotides, and characterizing and expressing clones in *E. coli*. Also constructed a general purpose expression vector for use by other scientific teams.

PUBLICATIONS

1. Hilary F. Clark, et al. "The Secreted Protein Discovery Initiative (SPDI), a Large-scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: a bioinformatics assessment." *Genome Res.* Vol 13(10), 2265-2270, 2003
2. Sean H. Adams, Clarissa Chui, Sarah L. Schilbach, Xing Xian Yu, Audrey D. Goddard, J. Christopher Grimaldi, James Lee, Patrick Dowd, David A. Lewin, & Steven Colman. "BFTT, a Unique Acyl-CoA Thioesterase Induced in Thermogenic Brown Adipose Tissue: Cloning, organization of the human gene and assessment of a potential link to obesity" *Biochemical Journal*, Vol 360, 135-142, 2001
3. Szeto W, Jiang W, Tice DA, Rubinfeld B, Hollingshead PG, Fong SE, Dugger DL, Pham T, Yansura D, Wong TA, Grimaldi JC, Corpuz RT, Singh JS, Frantz GD, Devaux B, Crowley CW, Schwall RH, Eberhard DA, Rastelli L, Polakis P, and Pennica D. "Overexpression of the Retenoic Acid-Responsive Gene *Stra6* in Human Cancers and its Synergistic Activation by Wnt-1 and Retinoic Acid." *Cancer Research* Vol. 61(10), 4197-4205, 2001
4. Jeanne Kahn, Fuad Mehraban, Gladdys Ingle, Xiaohua Xin, Juliet E. Bryant, Gordon Vehar, Jill Schoenfeld, J. Christopher Grimaldi (incorrectly named as "Grimaldi, CJ"), Franklin Peale, Aparna Draksharapu, David A. Lewin, and Mary E. Gerritsen. "Gene Expression Profiling in an in Vitro Model of Angiogenesis." *American Journal of Pathology* Vol 156(6), 1887-1900, 2000.
5. Grimaldi JC, Yu NX, Grunig G, Seymour BW, Cottrez F, Robinson DS, Hosken N, Ferlin WG, Wu X, Soto H, O'Garra A, Howard MC, Coffman RL. "Depletion of eosinophils in mice through the use of antibodies specific for C-C chemokine receptor 3 (CCR3). *Journal of Leukocyte Biology*; Vol. 65(6), 846-53, 1999
6. Oliver AM, Grimaldi JC, Howard MC, Kearney JF. "Independently ligating CD38 and Fc gammaRIIB relays a dominant negative signal to B cells." *Hybridoma* Vol. 18(2), 113-9, 1999

7. Cockayne DA, Muchamuel T, Grimaldi JC, Muller-Steffner H, Randall TD, Lund FE, Murray R, Schuber F, Howard MC. "Mice deficient for the ecto-nicotinamide adenine dinucleotide glycohydrolase CD38 exhibit altered humoral immune responses." *Blood* Vol. 92(4), 1324-33, 1998
8. Frances E. Lund, Nanette W. Solvason, Michael P. Cooke, Andrew W. Heath, J. Christopher Grimaldi, Troy D. Randall, R. M. E. Parkhouse, Christopher C Goodnow and Maureen C. Howard. "Signaling through murine CD38 is impaired in antigen receptor unresponsive B cells." *European Journal of Immunology*, Vol. 25(5), 1338-1345, 1995
9. M. J. Guimaraes, J. F. Bazan, A. Zolotnik, M. V. Wiles, J. C. Grimaldi, F. Lee, T. McClanahan. "A new approach to the study of haematopoietic development in the yolk sac and embryoid body." *Development*, Vol. 121(10), 3335-3346, 1995
10. J. Christopher Grimaldi, Sriram Balasubramanian, J. Fernando Bazan, Armen Shanafelt, Gerard Zurawski and Maureen Howard. "CD38-mediated protein ribosylation." *Journal of Immunology*, Vol. 155(2), 811-817, 1995
11. Leopoldo Santos-Argumedo, Frances F. Lund, Andrew W. Heath, Nanette Solvason, Wei Wei Wu, J. Christopher Grimaldi, R. M. E. Parkhouse and Maureen Howard. "CD38 unresponsiveness of xid B cells implicates Bruton's tyrosine kinase (btk) as a regulator of CD38 induced signal transduction." *International Immunology*, Vol 7(2), 163-170, 1995
12. Frances Lund, Nanette Solvason, J. Christopher Grimaldi, R. M. E. Parkhouse and Maureen Howard. "Murine CD38: An immunoregulatory ectoenzyme." *Immunology Today*, Vol: 16(10), 469-473, 1995
13. Maureen Howard, J. Christopher Grimaldi, J. Fernando Bazan, Frances E. Lund, Leopoldo Santos-Argumedo, R. M. E. Parkhouse, Timothy F. Walseth, and Hon Cheung Lee. "Formation and Hydrolysis of Cyclic ADP-Ribose Catalyzed by Lymphocyte Antigen CD38." *Science*, Vol. 262, 1056-1059, 1993
14. Nobuyuki Harada, Leopoldo Santos-Argumedo, Ray Chang, J. Christopher Grimaldi, Frances Lund, Camilynn I. Brannan, Neal G. Copeland, Nancy A. Jenkins, Andrew Heath, R. M. E. Parkhouse and Maureen Howard. "Expression Cloning of a cDNA Encoding a Novel Murine B Cell Activation Marker: Homology to Human CD38." *The Journal of Immunology*, Vol. 151, 3111-3118, 1993
15. David J. Rawlings, Douglas C. Saffran, Satoshi Tsukada, David A. Largaespada, J. Christopher Grimaldi, Lucie Cohen Randolph N. Mohr, J. Fernando Bazan, Maureen Howard, Neal G. Copeland, Nancy A. Jenkins, Owen Witte. "Mutation of Unique Region of Bruton's Tyrosine Kinase in Immunodeficient XID Mice." *Science*, Vol. 261, 358-360, 1993
16. J. Christopher Grimaldi, Raul Torres, Christine A. Kozak, Ray Chang, Edward Clark, Maureen Howard, and Debra A. Cockayne. "Genomic Structure and Chromosomal Mapping of the Murine CD40 Gene." *The Journal of Immunology*, Vol 149, 3921-3926, 1992
17. Timothy C. Meeker, Bruce Shiramizu, Lawrence Kaplan, Brian Herndier, Henry Sanchez, J. Christopher Grimaldi, James Baumgartner, Jacob Rachlin, Ellen Feigal, Mark Rosenblum and Michael S. McGrath. "Evidence for Molecular Subtypes of HIV-Associated Lymphoma:

Division into Peripheral Monoclonal, Polyclonal and Central Nervous System Lymphoma." AIDS, Vol. 5, 669-674, 1991

18. Ann Grimaldi and Chris Grimaldi. "Small-Scale Lambda DNA Prep." Contribution to Current Protocols in Molecular Biology, Supplement 5, Winter 1989
19. J. Christopher Grimaldi, Timothy C. Meeker. "The t(5;14) Chromosomal Translocation in a Case of Acute Lymphocytic Leukemia Joins the Interleukin-3 Gene to the Immunoglobulin Heavy Chain Gene." Blood, Vol. 73, 2081-2085, 1989
20. Timothy C. Meeker, J. Christopher Grimaldi, et al. "An Additional Breakpoint Region in the BCL-1 Locus Associated with the t(11;14) (q13;q32) Translocation of B-Lymphocytic Malignancy." Blood, Vol. 74, 1801-1806, 1989
21. Timothy C. Meeker, J. Christopher Grimaldi, Robert O'Rourke, et al. "Lack of Detectable Somatic Hypermutation in the V_H Region of the Ig H Chain Gene of a Human Chronic B Lymphocytic Leukemia." The Journal of Immunology, Vol. 141, 3994-3998, 1988

MANUSCRIPTS IN PREPARATION

1. Sriram Balasubramanian, J. Christopher Grimaldi, J. Fernando Bazan, Gerard Zurawski and Maureen Howard. "Structural and functional characterization of CD38: Identification of active site residues"

PATENTS

1. "Methods for Eosinophil Depletion with Antibody to CCR3 Receptor" (US 6,207,155 B1).
2. "Amplification Based Cloning Method." (US 6,607,899)
3. Ashkenazi et al., "Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same." (this patent covers several hundred genes)
4. "IL-17 Homologous Polypeptides and Therapeutic Uses Thereof"
5. "Method of Diagnosing and Treating Cartilaginous Disorders."

MEMBERSHIPS AND ACTIVITIES

Editor Frontiers in Bioscience

Member DNAX Safety Committee 1991-1999
 Biological Safety Affairs Forum (BSAF) 1990-1991
 Environmental Law Foundation (ELF) 1990-1991

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

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Examiner	:	David J. Blanchard
Group Art Unit	:	1642

DECLARATION OF J. CHRISTOPHER GRIMALDI, UNDER 37 C.F.R. § 1.132

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

I, J. Christopher Grimaldi, declare and say as follows:

1. I am a Senior Research Associate in the Molecular Biology Department of Genentech, Inc., South San Francisco, CA 94080.

2. I joined Genentech in January of 1999. From 1999 to 2003, I directed the Cloning Laboratory in the Molecular Biology Department. During this time I directed or performed numerous molecular biology techniques including qualitative Polymerase Chain Reaction (PCR) analyses. I am currently involved in, among other projects, the isolation of genes coding for membrane associated proteins which can be used as targets for antibody therapeutics against cancer. In connection with the above-identified patent application, I personally performed or directed the semi-quantitative PCR analyses in the assay entitled "Tumor Versus Normal Differential Tissue Expression Distribution" which is described in EXAMPLE 18 in the specification that were used to identify differences in gene expression between tumor tissue and their normal counterparts.

3. My scientific Curriculum Vitae, including my list of publications, is attached to and forms part of this Declaration (Exhibit A).

4. In differential gene expression studies, one looks for genes whose expression levels differ significantly under different conditions, for example, in normal versus diseased tissue.

Chromosomal aberrations, such as gene amplification, and chromosomal translocations are important markers of specific types of cancer and lead to the aberrant expression of specific genes and their encoded polypeptides, including over-expression and under-expression. For example, gene amplification is a process in which specific regions of a chromosome are duplicated, thus creating multiple copies of certain genes that normally exist as a single copy. Gene under-expression can occur when a gene is not transcribed into mRNA. In addition, chromosomal translocations occur when two different chromosomes break and are rejoined to each other chromosome resulting in a chimeric chromosome which displays a different expression pattern relative to the parent chromosomes. Amplification of certain genes such as Her2/Neu [Singleton *et al.*, Pathol. Annu., 27Pt1:165-190], or chromosomal translocations such as t(5;14), [Grimaldi *et al.*, Blood, 73(8):2081-2085(1989); Meeker *et al.*, Blood, 76(2):285-289(1990)] give cancer cells a growth or survival advantage relative to normal cells, and might also provide a mechanism of tumor cell resistance to chemotherapy or radiotherapy. When the chromosomal aberration results in the aberrant expression of a mRNA and the corresponding gene product (the polypeptide), as it does in the aforementioned cases, the gene product is a promising target for cancer therapy, for example, by the therapeutic antibody approach.

5. Comparison of gene expression levels in normal versus diseased tissue has important implications both diagnostically and therapeutically. For example, those who work in this field are well aware that in the vast majority of cases, when a gene is over-expressed, as evidenced by an increased production of mRNA, the gene product or polypeptide will also be over-expressed. It is unlikely that one identifies increased mRNA expression without associated increased protein expression. This same principle applies to gene under-expression. When a gene is under-expressed, the gene product is also likely to be under-expressed. Stated in another way, two cell samples which have differing mRNA concentrations for a specific gene are expected to have correspondingly different concentration of protein for that gene. Techniques used to detect mRNA, such as Northern Blotting, Differential Display, *in situ* hybridization, quantitative PCR, Taqman, and more recently Microarray technology all rely on the dogma that a change in mRNA will represent a similar change in protein. If this dogma did not hold true then these techniques would have little value and not be so widely used. The use of mRNA quantitation techniques have identified a seemingly endless number of genes which are differentially expressed in various tissues and these genes have subsequently been shown to have correspondingly similar changes in their protein levels. Thus, the detection of increased mRNA expression is expected to result in increased polypeptide expression, and the detection of decreased mRNA expression is expected to result in decreased polypeptide expression. The detection of increased or decreased polypeptide expression can be used for cancer diagnosis and treatment.

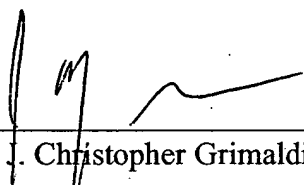
6. However, even in the rare case where the protein expression does not correlate with the mRNA expression, this still provides significant information useful for cancer diagnosis and treatment. For example, if over- or under-expression of a gene product does not correlate with over- or under-expression of mRNA in certain tumor types but does so in others, then identification of both gene expression and protein expression enables more accurate tumor classification and hence better determination of suitable therapy. In addition, absence of over- or

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under-expression of the gene product in the presence of a particular over- or under-expression of mRNA is crucial information for the practicing clinician. For example, if a gene is over-expressed but the corresponding gene product is not significantly over-expressed, the clinician accordingly will decide not to treat a patient with agents that target that gene product.

7. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

By:



Christopher Grimaldi

Date:

8/10/2001

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PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Botstein, et al.
Appl. No. : 10/032,996
Filed : December 27, 2001
For : SECRETED AND
TRANSMEMBRANE
POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME
Examiner : Fredman, J.
Group Art Unit : 1634

COPY

DECLARATION OF PAUL POLAKIS, PH.D. UNDER 37 C.F.R. § 1.132

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

Attached is the Declaration of Paul Polakis, Ph.D.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: June 14, 2004

By: AnneMarie Kaiser
AnneMarie Kaiser
Registration No. 37,649
Attorney of Record
Customer No. 30,313
(619) 235-8550

DECLARATION OF PAUL POLAKIS, Ph.D.

I, Paul Polakis, Ph.D., declare and say as follows:

1. I was awarded a Ph.D. by the Department of Biochemistry of the Michigan State University in 1984. My scientific Curriculum Vitae is attached to and forms part of this Declaration (Exhibit A).
2. I am currently employed by Genentech, Inc. where my job title is Staff Scientist. Since joining Genentech in 1999, one of my primary responsibilities has been leading Genentech's Tumor Antigen Project, which is a large research project with a primary focus on identifying tumor cell markers that find use as targets for both the diagnosis and treatment of cancer in humans.
3. As part of the Tumor Antigen Project, my laboratory has been analyzing differential expression of various genes in tumor cells relative to normal cells. The purpose of this research is to identify proteins that are abundantly expressed on certain tumor cells and that are either (i) not expressed, or (ii) expressed at lower levels, on corresponding normal cells. We call such differentially expressed proteins "tumor antigen proteins". When such a tumor antigen protein is identified, one can produce an antibody that recognizes and binds to that protein. Such an antibody finds use in the diagnosis of human cancer and may ultimately serve as an effective therapeutic in the treatment of human cancer.
4. In the course of the research conducted by Genentech's Tumor Antigen Project, we have employed a variety of scientific techniques for detecting and studying differential gene expression in human tumor cells relative to normal cells, at genomic DNA, mRNA and protein levels. An important example of one such technique is the well known and widely used technique of microarray analysis which has proven to be extremely useful for the identification of mRNA molecules that are differentially expressed in one tissue or cell type relative to another. In the course of our research using microarray analysis, we have identified approximately 200 gene transcripts that are present in human tumor cells at significantly higher levels than in corresponding normal human cells. To date, we have generated antibodies that bind to about 30 of the tumor antigen proteins expressed from these differentially expressed gene transcripts and have used these antibodies to quantitatively determine the level of production of these tumor antigen proteins in both human cancer cells and corresponding normal cells. We have then compared the levels of mRNA and protein in both the tumor and normal cells analyzed.
5. From the mRNA and protein expression analyses described in paragraph 4 above, we have observed that there is a strong correlation between changes in the level of mRNA present in any particular cell type and the level of protein

expressed from that mRNA in that cell type. In approximately 80% of our observations we have found that increases in the level of a particular mRNA correlates with changes in the level of protein expressed from that mRNA when human tumor cells are compared with their corresponding normal cells.

6. Based upon my own experience accumulated in more than 20 years of research, including the data discussed in paragraphs 4 and 5 above and my knowledge of the relevant scientific literature, it is my considered scientific opinion that for human genes, an increased level of mRNA in a tumor cell relative to a normal cell typically correlates to a similar increase in abundance of the encoded protein in the tumor cell relative to the normal cell. In fact, it remains a central dogma in molecular biology that increased mRNA levels are predictive of corresponding increased levels of the encoded protein. While there have been published reports of genes for which such a correlation does not exist, it is my opinion that such reports are exceptions to the commonly understood general rule that increased mRNA levels are predictive of corresponding increased levels of the encoded protein.

7. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

Dated: 5/07/04

By: Paul Polakis

Paul Polakis, Ph.D.

CURRICULUM VITAE

PAUL G. POLAKIS
Staff Scientist
Genentech, Inc
1 DNA Way, MS#40
S. San Francisco, CA 94080

EDUCATION:

Ph.D., Biochemistry, Department of Biochemistry,
Michigan State University (1984)

B.S., Biology. College of Natural Science, Michigan State University (1977)

PROFESSIONAL EXPERIENCE:

2002-present	Staff Scientist, Genentech, Inc S. San Francisco, CA
1999- 2002	Senior Scientist, Genentech, Inc., S. San Francisco, CA
1997 -1999	Research Director Onyx Pharmaceuticals, Richmond, CA
1992- 1996	Senior Scientist, Project Leader, Onyx Pharmaceuticals, Richmond, CA
1991-1992	Senior Scientist, Chiron Corporation, Emeryville, CA.
1989-1991	Scientist, Cetus Corporation, Emeryville CA.
1987-1989	Postdoctoral Research Associate, Genentech, Inc., South San Francisco, CA.
1985-1987	Postdoctoral Research Associate, Department of Medicine, Duke University Medical Center, Durham, NC

1984-1985

Assistant Professor, Department of Chemistry,
Oberlin College, Oberlin, Ohio

1980-1984

Graduate Research Assistant, Department of
Biochemistry, Michigan State University
East Lansing, Michigan

PUBLICATIONS:

1. **Polakis, P. G.** and Wilson, J. E. 1982 Purification of a Highly Bindable Rat Brain Hexokinase by High Performance Liquid Chromatography. **Biochem. Biophys. Res. Commun.** 107, 937-943.
2. **Polakis, P.G.** and Wilson, J. E. 1984 Proteolytic Dissection of Rat Brain Hexokinase: Determination of the Cleavage Pattern during Limited Digestion with Trypsin. **Arch. Biochem. Biophys.** 234, 341-352.
3. **Polakis, P. G.** and Wilson, J. E. 1985 An Intact Hydrophobic N-Terminal Sequence is Required for the Binding Rat Brain Hexokinase to Mitochondria. **Arch. Biochem. Biophys.** 236, 328-337.
4. Uhing, R.J., **Polakis, P.G.** and Snyderman, R. 1987 Isolation of GTP-binding Proteins from Myeloid HL60 Cells. **J. Biol. Chem.** 262, 15575-15579.
5. **Polakis, P.G.**, Uhing, R.J. and Snyderman, R. 1988 The Formylpeptide Chemoattractant Receptor Copurifies with a GTP-binding Protein Containing a Distinct 40 kDa Pertussis Toxin Substrate. **J. Biol. Chem.** 263, 4969-4979.
6. Uhing, R. J., Dillon, S., **Polakis, P. G.**, Truett, A. P. and Snyderman, R. 1988 Chemoattractant Receptors and Signal Transduction Processes in Cellular and Molecular Aspects of Inflammation (Poste, G. and Crooke, S. T. eds.) pp 335-379.
7. **Polakis, P.G.**, Evans, T. and Snyderman 1989 Multiple Chromatographic Forms of the Formylpeptide Chemoattractant Receptor and their Relationship to GTP-binding Proteins. **Biochem. Biophys. Res. Commun.** 161, 276-283.
8. **Polakis, P. G.**, Snyderman, R. and Evans, T. 1989 Characterization of G25K, a GTP-binding Protein Containing a Novel Putative Nucleotide Binding Domain. **Biochem. Biophys. Res. Commun.** 160, 25-32.
9. **Polakis, P.**, Weber, R.F., Nevins, B., Didsbury, J. Evans, T. and Snyderman, R. 1989 Identification of the ral and rac1 Gene Products, Low Molecular Mass GTP-binding Proteins from Human Platelets. **J. Biol. Chem.** 264, 16383-16389.
10. Snyderman, R., Perianin, A., Evans, T., **Polakis, P.** and Didsbury, J. 1989 G Proteins and Neutrophil Function. In ADP-Ribosylating Toxins and G Proteins: Insights into Signal Transduction. (J. Moss and M. Vaughn, eds.) Amer. Soc. Microbiol. pp. 295-323.

11. Hart, M.J., Polakis, P.G., Evans, T. and Cerrione, R.A. 1990 The Identification and Characterization of an Epidermal Growth Factor-Stimulated Phosphorylation of a Specific Low Molecular Mass GTP-binding Protein in a Reconstituted Phospholipid Vesicle System. *J. Biol. Chem.* 265, 5990-6001.

12. Yatani, A., Okabe, K., Polakis, P., Halenbeck, R., McCormick, F. and Brown, A. M. 1990 ras p21 and GAP Inhibit Coupling of Muscarinic Receptors to Atrial K⁺ Channels. *Cell*. 61, 769-776.

13. Munemitsu, S., Innis, M.A., Clark, R., McCormick, F., Ullrich, A. and Polakis, P.G. 1990 Molecular Cloning and Expression of a G25K cDNA, the Human Homolog of the Yeast Cell Cycle Gene CDC42. *Mol. Cell. Biol.* 10, 5977-5982.

14. Polakis, P.G., Rubinfeld, B., Evans, T. and McCormick, F. 1991 Purification of Plasma Membrane-Associated GTPase Activating Protein (GAP) Specific for rap-1/krev-1 from HL60 Cells. *Proc. Natl. Acad. Sci. USA* 88, 239-243.

15. Moran, M. F., Polakis, P., McCormick, F., Pawson, T. and Ellis, C. 1991 Protein Tyrosine Kinases Regulate the Phosphorylation, Protein Interactions, Subcellular Distribution, and Activity of p21ras GTPase Activating Protein. *Mol. Cell. Biol.* 11, 1804-1812

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MOLECULAR BIOLOGY OF
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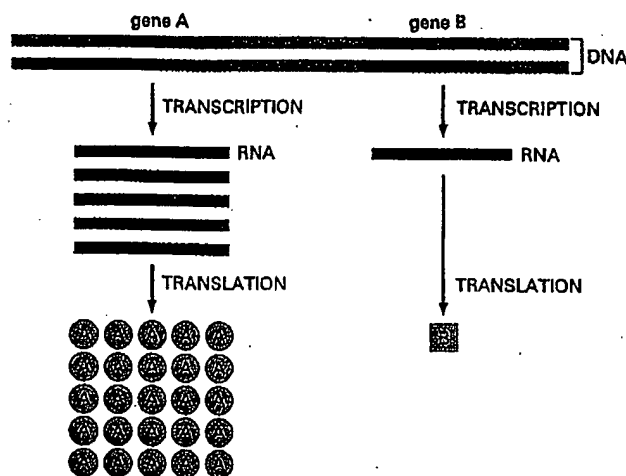


Figure 6-3 Genes can be expressed with different efficiencies. Gene A is transcribed and translated much more efficiently than gene B. This allows the amount of protein A in the cell to be much greater than that of protein B.

FROM DNA TO RNA

Transcription and translation are the means by which cells read out, or express, the genetic instructions in their genes. Because many identical RNA copies can be made from the same gene, and each RNA molecule can direct the synthesis of many identical protein molecules, cells can synthesize a large amount of protein rapidly when necessary. But each gene can also be transcribed and translated with a different efficiency, allowing the cell to make vast quantities of some proteins and tiny quantities of others (Figure 6-3). Moreover, as we see in the next chapter, a cell can change (or regulate) the expression of each of its genes according to the needs of the moment—most obviously by controlling the production of its RNA.

Portions of DNA Sequence Are Transcribed into RNA

The first step a cell takes in reading out a needed part of its genetic instructions is to copy a particular portion of its DNA nucleotide sequence—a gene—into an RNA nucleotide sequence. The information in RNA, although copied into another chemical form, is still written in essentially the same language as it is in DNA—the language of a nucleotide sequence. Hence the name **transcription**.

Like DNA, RNA is a linear polymer made of four different types of nucleotide subunits linked together by phosphodiester bonds (Figure 6-4). It differs from DNA chemically in two respects: (1) the nucleotides in RNA are *ribonucleotides*—that is, they contain the sugar ribose (hence the name *ribonucleic acid*) rather than deoxyribose; (2) although, like DNA, RNA contains the bases adenine (A), guanine (G), and cytosine (C), it contains the base uracil (U) instead of the thymine (T) in DNA. Since U, like T, can base-pair by hydrogen-bonding with A (Figure 6-5), the complementary base-pairing properties described for DNA in Chapters 4 and 5 apply also to RNA (in RNA, G pairs with C, and A pairs with U). It is not uncommon, however, to find other types of base pairs in RNA: for example, G pairing with U occasionally.

Despite these small chemical differences, DNA and RNA differ quite dramatically in overall structure. Whereas DNA always occurs in cells as a double-stranded helix, RNA is single-stranded. RNA chains therefore fold up into a variety of shapes, just as a polypeptide chain folds up to form the final shape of a protein (Figure 6-6). As we see later in this chapter, the ability to fold into complex three-dimensional shapes allows some RNA molecules to have structural and catalytic functions.

Transcription Produces RNA Complementary to One Strand of DNA

All of the RNA in a cell is made by DNA transcription, a process that has certain similarities to the process of DNA replication discussed in Chapter 5.

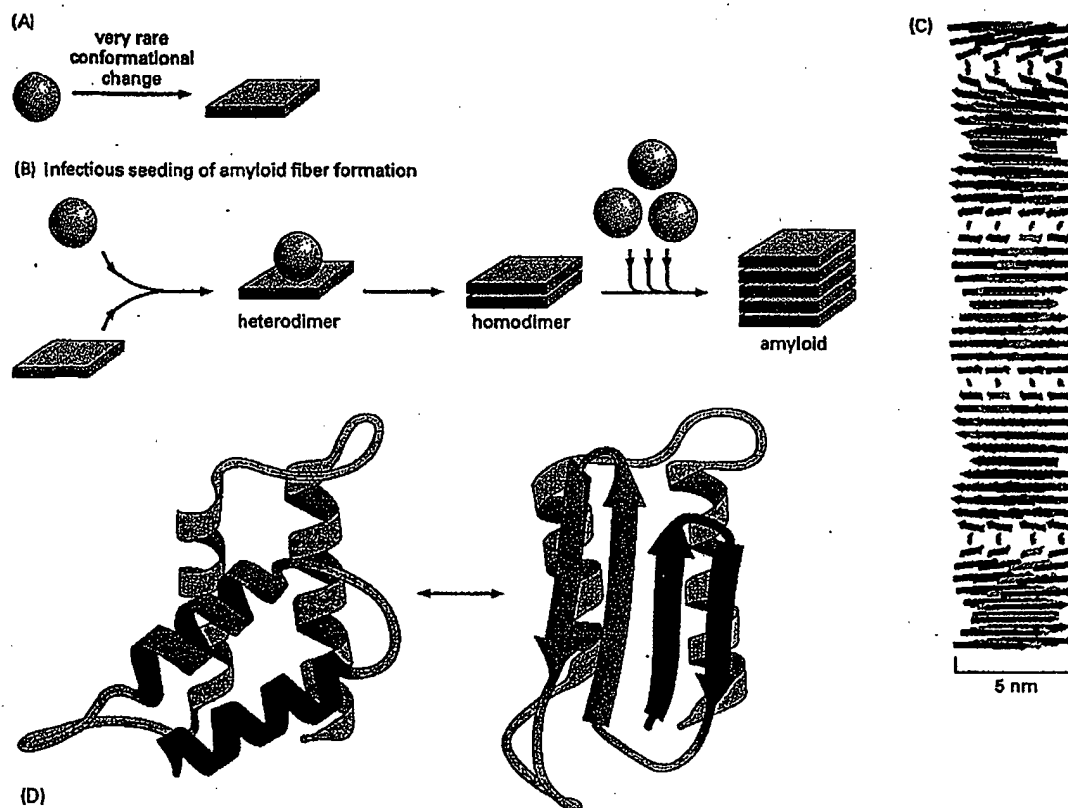


Figure 6-89 Protein aggregates that cause human disease. (A) Schematic illustration of the type of conformational change in a protein that produces material for a cross-beta filament. (B) Diagram illustrating the self-infectious nature of the protein aggregation that is central to prion diseases. PrP is highly unusual because the misfolded version of the protein, called PrP^{*}, induces the normal PrP protein it contacts to change its conformation, as shown. Most of the human diseases caused by protein aggregation are caused by the overproduction of a variant protein that is especially prone to aggregation, but because this structure is not infectious in this way, it cannot spread from one animal to another. (C) Drawing of a cross-beta filament, a common type of protease-resistant protein aggregate found in a variety of human neurological diseases. Because the hydrogen-bond interactions in a β sheet form between polypeptide backbone atoms (see Figure 3-9), a number of different abnormally folded proteins can produce this structure. (D) One of several possible models for the conversion of PrP to PrP^{*}, showing the likely change of two α -helices into four β -strands. Although the structure of the normal protein has been determined accurately, the structure of the infectious form is not yet known with certainty because the aggregation has prevented the use of standard structural techniques. (C, courtesy of Louise Serpell, adapted from M. Sunde et al., *J. Mol. Biol.* 273:729-739, 1997; D, adapted from S.B. Prusiner, *Trends Biochem. Sci.* 21:482-487, 1996.)

animals and humans. It can be dangerous to eat the tissues of animals that contain PrP^{*}, as witnessed most recently by the spread of BSE (commonly referred to as the "mad cow disease") from cattle to humans in Great Britain.

Fortunately, in the absence of PrP^{*}, PrP is extraordinarily difficult to convert to its abnormal form. Although very few proteins have the potential to misfold into an infectious conformation, a similar transformation has been discovered to be the cause of an otherwise mysterious "protein-only inheritance" observed in yeast cells.

There Are Many Steps From DNA to Protein

We have seen so far in this chapter that many different types of chemical reactions are required to produce a properly folded protein from the information contained in a gene (Figure 6-90). The final level of a properly folded protein in a cell therefore depends upon the efficiency with which each of the many steps is performed.

We discuss in Chapter 7 that cells have the ability to change the levels of their proteins according to their needs. In principle, any or all of the steps in Fig-

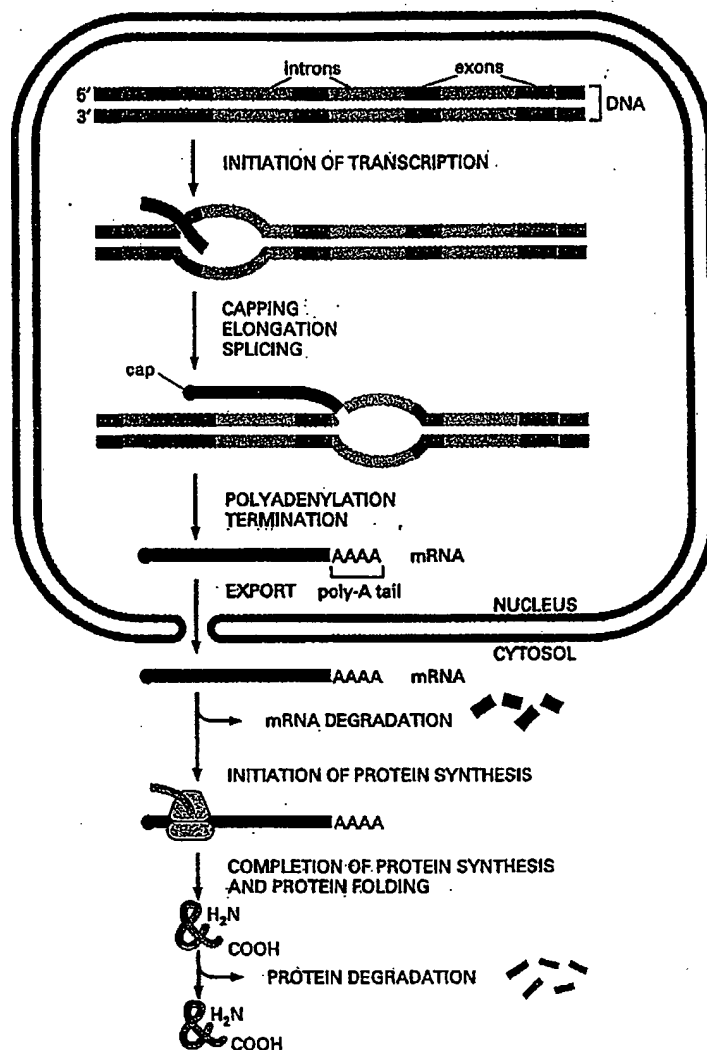


Figure 6-90 The production of a protein by a eucaryotic cell. The final level of each protein in a eucaryotic cell depends upon the efficiency of each step depicted.

ure 6-90) could be regulated by the cell for each individual protein. However, as we shall see in Chapter 7, the initiation of transcription is the most common point for a cell to regulate the expression of each of its genes. This makes sense, inasmuch as the most efficient way to keep a gene from being expressed is to block the very first step—the transcription of its DNA sequence into an RNA molecule.

Summary

The translation of the nucleotide sequence of an mRNA molecule into protein takes place in the cytoplasm on a large ribonucleoprotein assembly called a ribosome. The amino acids used for protein synthesis are first attached to a family of tRNA molecules, each of which recognizes, by complementary base-pair interactions, particular sets of three nucleotides in the mRNA (codons). The sequence of nucleotides in the mRNA is then read from one end to the other in sets of three according to the genetic code.

To initiate translation, a small ribosomal subunit binds to the mRNA molecule at a start codon (AUG) that is recognized by a unique initiator tRNA molecule. A large ribosomal subunit binds to complete the ribosome and begin the elongation phase of protein synthesis. During this phase, aminoacyl tRNAs—each bearing a specific amino acid bind sequentially to the appropriate codon in mRNA by forming complementary base pairs with the tRNA anticodon. Each amino acid is added to the C-terminal end of the growing polypeptide by means of a cycle of three sequential

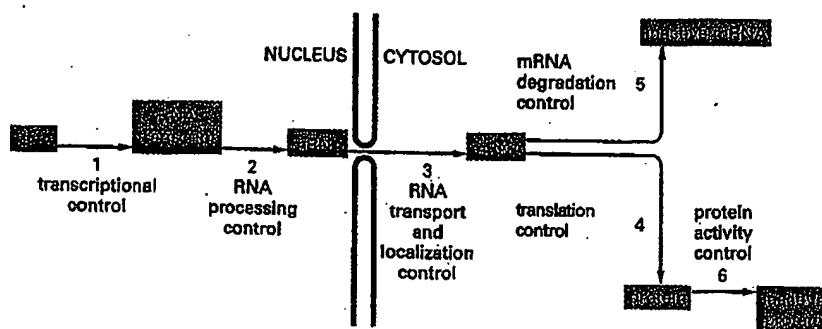


Figure 7-5 Six steps at which eucaryotic gene expression can be controlled. Controls that operate at steps 1 through 5 are discussed in this chapter. Step 6, the regulation of protein activity, includes reversible activation or inactivation by protein phosphorylation (discussed in Chapter 3) as well as irreversible inactivation by proteolytic degradation (discussed in Chapter 6).

Gene Expression Can Be Regulated at Many of the Steps in the Pathway from DNA to RNA to Protein

If differences among the various cell types of an organism depend on the particular genes that the cells express, at what level is the control of gene expression exercised? As we saw in the last chapter, there are many steps in the pathway leading from DNA to protein, and all of them can in principle be regulated. Thus a cell can control the proteins it makes by (1) controlling when and how often a given gene is transcribed (**transcriptional control**), (2) controlling how the RNA transcript is spliced or otherwise processed (**RNA processing control**), (3) selecting which completed mRNAs in the cell nucleus are exported to the cytosol and determining where in the cytosol they are localized (**RNA transport and localization control**), (4) selecting which mRNAs in the cytoplasm are translated by ribosomes (**translational control**), (5) selectively destabilizing certain mRNA molecules in the cytoplasm (**mRNA degradation control**), or (6) selectively activating, inactivating, degrading, or compartmentalizing specific protein molecules after they have been made (**protein activity control**) (Figure 7-5).

For most genes transcriptional controls are paramount. This makes sense because, of all the possible control points illustrated in Figure 7-5, only transcriptional control ensures that the cell will not synthesize superfluous intermediates. In the following sections we discuss the DNA and protein components that perform this function by regulating the initiation of gene transcription. We shall return at the end of the chapter to the additional ways of regulating gene expression.

Summary

The genome of a cell contains in its DNA sequence the information to make many thousands of different protein and RNA molecules. A cell typically expresses only a fraction of its genes, and the different types of cells in multicellular organisms arise because different sets of genes are expressed. Moreover, cells can change the pattern of genes they express in response to changes in their environment, such as signals from other cells. Although all of the steps involved in expressing a gene can in principle be regulated, for most genes the initiation of RNA transcription is the most important point of control.

DNA-BINDING MOTIFS IN GENE REGULATORY PROTEINS

How does a cell determine which of its thousands of genes to transcribe? As mentioned briefly in Chapters 4 and 6, the transcription of each gene is controlled by a regulatory region of DNA relatively near the site where transcription begins. Some regulatory regions are simple and act as switches that are thrown by a single signal. Many others are complex and act as tiny microprocessors, responding to a variety of signals that they interpret and integrate to switch the neighboring gene on or off. Whether complex or simple, these switching devices

occur in the germ line, the cell lineage that gives rise to sperm or eggs. Most of the DNA in vertebrate germ cells is inactive and highly methylated. Over long periods of evolutionary time, the methylated CG sequences in these inactive regions have presumably been lost through spontaneous deamination events that were not properly repaired. However promoters of genes that remain active in the germ cell lineages (including most housekeeping genes) are kept unmethylated, and therefore spontaneous deaminations of Cs that occur within them can be accurately repaired. Such regions are preserved in modern day vertebrate cells as CG islands. In addition, any mutation of a CG sequence in the genome that destroyed the function or regulation of a gene in the adult would be selected against, and some CG islands are simply the result of a higher than normal density of critical CG sequences.

The mammalian genome contains an estimated 20,000 CG islands. Most of the islands mark the 5' ends of transcription units and thus, presumably, of genes. The presence of CG islands often provides a convenient way of identifying genes in the DNA sequences of vertebrate genomes.

Summary

The many types of cells in animals and plants are created largely through mechanisms that cause different genes to be transcribed in different cells. Since many specialized animal cells can maintain their unique character through many cell division cycles and even when grown in culture, the gene regulatory mechanisms involved in creating them must be stable once established and heritable when the cell divides. These features endow the cell with a memory of its developmental history. Bacteria and yeasts provide unusually accessible model systems in which to study gene regulatory mechanisms. One such mechanism involves a competitive interaction between two gene regulatory proteins, each of which inhibits the synthesis of the other; this can create a flip-flop switch that switches a cell between two alternative patterns of gene expression. Direct or indirect positive feedback loops, which enable gene regulatory proteins to perpetuate their own synthesis, provide a general mechanism for cell memory. Negative feedback loops with programmed delays form the basis for cellular clocks.

In eucaryotes the transcription of a gene is generally controlled by combinations of gene regulatory proteins. It is thought that each type of cell in a higher eucaryotic organism contains a specific combination of gene regulatory proteins that ensures the expression of only those genes appropriate to that type of cell. A given gene regulatory protein may be active in a variety of circumstances and typically is involved in the regulation of many genes.

In addition to diffusible gene regulatory proteins, inherited states of chromatin condensation are also used by eucaryotic cells to regulate gene expression. An especially dramatic case is the inactivation of an entire X chromosome in female mammals. In vertebrates DNA methylation also functions in gene regulation, being used mainly as a device to reinforce decisions about gene expression that are made initially by other mechanisms. DNA methylation also underlies the phenomenon of genomic imprinting in mammals, in which the expression of a gene depends on whether it was inherited from the mother or the father.

POSTTRANSCRIPTIONAL CONTROLS

In principle, every step required for the process of gene expression could be controlled. Indeed, one can find examples of each type of regulation, although any one gene is likely to use only a few of them. Controls on the initiation of gene transcription are the predominant form of regulation for most genes. But other controls can act later in the pathway from DNA to protein to modulate the amount of gene product that is made. Although these posttranscriptional controls, which operate after RNA polymerase has bound to the gene's promoter and begun RNA synthesis, are less common than transcriptional control, for many genes they are crucial.

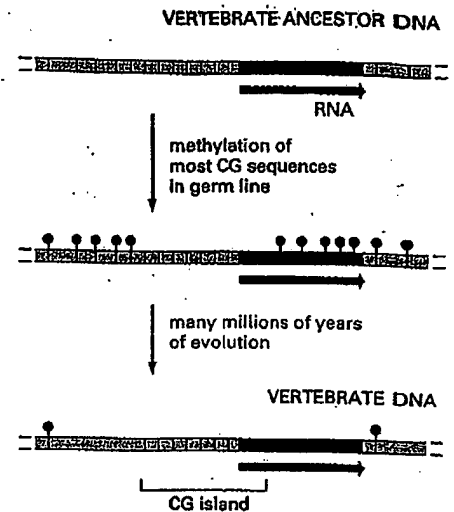


Figure 7-86 A mechanism to explain both the marked overall deficiency of CG sequences and their clustering into CG islands in vertebrate genomes. A black line marks the location of a CG dinucleotide in the DNA sequence, while a red "lollipop" indicates the presence of a methyl group on the CG dinucleotide. CG sequences that lie in regulatory sequences of genes that are transcribed in germ cells are unmethylated and therefore tend to be retained in evolution. Methylated CG sequences, on the other hand, tend to be lost through deamination of 5-methyl C to T, unless the CG sequence is critical for survival.

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Ashkenazi et al.

App. No. : 09/903,925

Filed : July 11, 2001

For : **SECRETED AND
TRANSMEMBRANE
POLYPEPTIDES AND NUCLEIC
ACIDS ENCODING THE SAME**

Examiner : Hamud, Fozia M

Group Art Unit 1647

CERTIFICATE OF EXPRESS MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to Commissioner of Patents, Washington D.C. 20231 on:

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DECLARATION OF AVI ASHKENAZI, Ph.D UNDER 37 C.F.R. § 1.132

I, Avi Ashkenazi, Ph.D. declare and say as follows: -

1. I am Director and Staff Scientist at the Molecular Oncology Department of Genentech, Inc., South San Francisco, CA 94080.
2. I joined Genentech in 1988 as a postdoctoral fellow. Since then, I have investigated a variety of cellular signal transduction mechanisms, including apoptosis, and have developed technologies to modulate such mechanisms as a means of therapeutic intervention in cancer and autoimmune disease. I am currently involved in the investigation of a series of secreted proteins over-expressed in tumors, with the aim to identify useful targets for the development of therapeutic antibodies for cancer treatment.
3. My scientific Curriculum Vitae, including my list of publications, is attached to and forms part of this Declaration (Exhibit A).
4. Gene amplification is a process in which chromosomes undergo changes to contain multiple copies of certain genes that normally exist as a single copy, and is an important factor in the pathophysiology of cancer. Amplification of certain genes (e.g., Myc or Her2/Neu)

gives cancer cells a growth or survival advantage relative to normal cells, and might also provide a mechanism of tumor cell resistance to chemotherapy or radiotherapy.

5. If gene amplification results in over-expression of the mRNA and the corresponding gene product, then it identifies that gene product as a promising target for cancer therapy, for example by the therapeutic antibody approach. Even in the absence of over-expression of the gene product, amplification of a cancer marker gene - as detected, for example, by the reverse transcriptase TaqMan[®] PCR or the fluorescence *in situ* hybridization (FISH) assays - is useful in the diagnosis or classification of cancer, or in predicting or monitoring the efficacy of cancer therapy. An increase in gene copy number can result not only from intrachromosomal changes but also from chromosomal aneuploidy. It is important to understand that detection of gene amplification can be used for cancer diagnosis even if the determination includes measurement of chromosomal aneuploidy. Indeed, as long as a significant difference relative to normal tissue is detected, it is irrelevant if the signal originates from an increase in the number of gene copies per chromosome and/or an abnormal number of chromosomes.

6. I understand that according to the Patent Office, absent data demonstrating that the increased copy number of a gene in certain types of cancer leads to increased expression of its product, gene amplification data are insufficient to provide substantial utility or well established utility for the gene product (the encoded polypeptide), or an antibody specifically binding the encoded polypeptide. However, even when amplification of a cancer marker gene does not result in significant over-expression of the corresponding gene product, this very absence of gene product over-expression still provides significant information for cancer diagnosis and treatment. Thus, if over-expression of the gene product does not parallel gene amplification in certain tumor types but does so in others, then parallel monitoring of gene amplification and gene product over-expression enables more accurate tumor classification and hence better determination of suitable therapy. In addition, absence of over-expression is crucial information for the practicing clinician. If a gene is amplified but the corresponding gene product is not over-expressed, the clinician accordingly will decide not to treat a patient with agents that target that gene product.

7. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so

made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

By: Avi Ashkenazi
Avi Ashkenazi, Ph.D.

Date: 9/15/03

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CURRICULUM VITAE

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July 2003

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Education:

1983: B.S. in Biochemistry, with honors, Hebrew University, Israel
1986: Ph.D. in Biochemistry, Hebrew University, Israel

Employment:

1983-1986: Teaching assistant, undergraduate level course in Biochemistry
1985-1986: Teaching assistant, graduate level course on Signal Transduction
1986 - 1988: Postdoctoral fellow, Hormone Research Dept., UCSF, and
Developmental Biology Dept., Genentech, Inc., with J. Ramachandran
1988 - 1989: Postdoctoral fellow, Molecular Biology Dept., Genentech, Inc.,
with D. Capon
1989 - 1993: Scientist, Molecular Biology Dept., Genentech, Inc.
1994 -1996: Senior Scientist, Molecular Oncology Dept., Genentech, Inc.
1996-1997: Senior Scientist and Interim director, Molecular Oncology Dept.,
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1997-1990: Senior Scientist and preclinical project team leader, Genentech, Inc.
1999 -2002: Staff Scientist in Molecular Oncology, Genentech, Inc.
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Awards:

1988: First prize, The Boehringer Ingelheim Award

Editorial:

Editorial Board Member: Current Biology

Associate Editor, Clinical Cancer Research.

Associate Editor, Cancer Biology and Therapy.

Refereed papers:

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Review articles:

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TECHNICAL UPDATE

FROM YOUR LABORATORY SERVICES PROVIDER

HER-2/neu Breast Cancer Predictive Testing

Julie Sanford Hanna, Ph.D. and Dan Mornin, M.D.

EACH YEAR, OVER 182,000 WOMEN in the United States are diagnosed with breast cancer, and approximately 45,000 die of the disease.¹ Incidence appears to be increasing in the United States at a rate of roughly 2% per year. The reasons for the increase are unclear, but non-genetic risk factors appear to play a large role.²

Five-year survival rates range from approximately 65%-85%, depending on demographic group, with a significant percentage of women experiencing recurrence of their cancer within 10 years of diagnosis. One of the factors most predictive for recurrence once a diagnosis of breast cancer has been made is the number of axillary lymph nodes to which tumor has metastasized. Most node-positive women are given adjuvant therapy, which increases their survival. However, 20%-30% of patients without axillary-node involvement also develop recurrent disease, and the difficulty lies in how to identify this high-risk subset of patients. These patients could benefit from increased surveillance, early intervention, and treatment.

Prognostic markers currently used in breast cancer recurrence prediction include tumor size, histological grade, steroid hormone receptor status, DNA ploidy, proliferative index, and cathepsin D status. Expression of growth factor receptors and over-expression of the HER-2/neu oncogene have also been identified as having value regarding treatment regimen and prognosis.

HER-2/neu (also known as c-erbB2) is an oncogene that encodes a transmembrane glycoprotein that is homologous to, but distinct from, the epidermal growth factor receptor. Numerous studies have indicated that high levels of expression of this protein are associated with rapid tumor growth, certain forms of therapy resistance, and shorter disease-free survival. The gene has been shown to be amplified and/or overexpressed in 10%-30% of invasive breast cancers and in 40%-60% of intraductal breast carcinoma.³

There are two distinct FDA-approved methods by which HER-2/neu status can be evaluated: immunohistochemistry (IHC, HercepTest™) and FISH (fluorescent in situ hybridization, PathVysion™ Kit). Both methods can be performed on archived and current specimens. The first method allows visual assessment of the amount of HER-2/neu protein present on the cell membrane. The latter method allows direct quantification of the level of gene amplification present in the tumor, enabling differentiation between low- versus high-amplification. At least one study has demonstrated a difference in

recurrence risk in women younger than 40 years of age for low- versus high-amplified tumors (54.5% compared to 85.7%); this is compared to a recurrence rate of 16.7% for patients with no HER-2/neu gene amplification.⁴ HER-2/neu status may be particularly important to establish in women with small (≤ 1 cm) tumor size.

The choice of methodology for determination of HER-2/neu status depends in part on the clinical setting. FDA approval for the Vysis FISH test was granted based on clinical trials involving 1549 node-positive patients. Patients received one of three different treatments consisting of different doses of cyclophosphamide, Adriamycin, and 5-fluorouracil (CAF). The study showed that patients with amplified HER-2/neu benefited from treatment with higher doses of adriamycin-based therapy, while those with normal HER-2/neu levels did not. The study therefore identified a sub-set of women, who because they did not benefit from more aggressive treatment, did not need to be exposed to the associated side effects. In addition, other evidence indicates that HER-2/neu amplification in node-negative patients can be used as an independent prognostic indicator for early recurrence, recurrent disease at any time and disease-related death.⁵ Demonstration of HER-2/neu gene amplification by FISH has also been shown to be of value in predicting response to chemotherapy in stage-2 breast cancer patients.

Selection of patients for Herceptin® (Trastuzumab) monoclonal antibody therapy, however, is based upon demonstration of HER-2/neu protein overexpression using HercepTest™. Studies using Herceptin® in patients with metastatic breast cancer show an increase in time to disease progression, increased response rate to chemotherapeutic agents and a small increase in overall survival rate. The FISH assays have not yet been approved for this purpose, and studies looking at response to Herceptin® in patients with or without gene amplification status determined by FISH are in progress.

In general, FISH and IHC results correlate well. However, subsets of tumors are found which show discordant results; i.e., protein overexpression without gene amplification or lack of protein overexpression with gene amplification. The clinical significance of such results is unclear. Based on the above considerations, HER-2/neu testing at SHMC/PAML will utilize immunohistochemistry (HercepTest®) as a screen, followed by FISH in IHC-negative cases. Alternatively, either method may be ordered individually depending on the clinical setting or clinician preference.

CPT code information

HER-2/neu via IHC

88342 (including interpretive report)

HER-2/neu via FISH

88271x2 Molecular cytogenetics, DNA probe, each

88274 Molecular cytogenetics, interphase in situ hybridization, analyze 25-99 cells

88291 Cytogenetics and molecular cytogenetics, interpretation and report

Procedural Information

Immunohistochemistry is performed using the FDA-approved DAKO antibody kit, Herceptest®. The DAKO kit contains reagents required to complete a two-step immunohistochemical staining procedure for routinely processed, paraffin-embedded specimens. Following incubation with the primary rabbit antibody to human HER-2/neu protein, the kit employs a ready-to-use dextran-based visualization reagent. This reagent consists of both secondary goat anti-rabbit antibody molecules with horseradish peroxidase molecules linked to a common dextran polymer backbone, thus eliminating the need for sequential application of link antibody and peroxidase conjugated antibody. Enzymatic conversion of the subsequently added chromogen results in formation of visible reaction product at the antigen site. The specimen is then counterstained; a pathologist using light-microscopy interprets results.

FISH analysis at SHMC/PAML is performed using the FDA-approved PathVysion™ HER-2/neu DNA probe kit, produced by Vysis, Inc. Formalin fixed, paraffin-embedded breast tissue is processed using routine histological methods, and then slides are treated to allow hybridization of DNA probes to the nuclei present in the tissue section. The Pathvysion™ kit contains two direct-labeled DNA probes, one specific for the aliphoid repetitive DNA (CEP 17, spectrum orange) present at the chromosome 17 centromere and the second for the HER-2/neu oncogene located at 17q11.2-12 (spectrum green). Enumeration of the probes allows a ratio of the number of copies of chromosome 17 to the number of copies of HER-2/neu to be obtained; this enables quantification of low versus high amplification levels, and allows an estimate of the percentage of cells with HER-2/neu gene amplification. The clinically relevant distinction is whether the gene amplification is due to increased gene copy number on the two chromosome 17 homologues normally present or an increase in the number of chromosome 17s in the cells. In the majority of cases, ratio equivalents less than 2.0 are indicative of a normal/negative result, ratios of 2.1 and over indicate that amplification is present and to what degree. Interpretation of this data will be performed and reported from the Vysis-certified Cytogenetics laboratory at SHMC.

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your local representative.*

<first sequence: ss.P_AAH25131 (length = 1909)

<second sequence: ss.DNA77626 (length = 1505)

<1504 matches in an overlap of 1505: 99.93 percent similarity

<gaps in first sequence: 0, gaps in second sequence: 1 (1 base)

<score: 4503 (match = 3, mismatch = 0, gap penalty = 8 + 1 per base)

<endgaps not penalized

GenBank (Release 143, aug 2004) [Dec 23 10:21:38 2004]: 1 sequence found

P_AAH25131 Nucleotide sequence of human alcohol dehydrogenase 21620. 909 bp,
DNA, PAT 22-AUG-2001
ACCESSION P_AAH25131
KEYWORDS GENESEQ; Human; alcohol dehydrogenase; colon disorder; brain
disorder; skin disorder; heart disorder; blood vessel disorder;
kidney disorder; prostate disorder; skeletal muscle disorder; ovary
disorder; testis disorder; epididymis disorder; spleen disorder;
lung disorder; liver disorder; uterus disorder; endometrium
disorder; T-cell disorder; red cell disorder; thymus disorder; B
cell disorder; breast disorder; thyroid disorder; pancreas disorder;
small intestine disorder; reduced platelet number disorder;
precursor T cell neoplasm; patent; patentdb (v200425, 02-DEC-2004).
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 1909)
AUTHORS Meyers,R.
TITLE Novel human alcohol dehydrogenase proteins, 21612, 21615, 21620,
21676, 33756, useful for treating psoriasis, tropical sprue,
pancreatitis, goiter, osteomalacia, endometriosis, angina pectoris,
embolism.
JOURNAL Patent: WO200144446-A2; Filing Date: 15-DEC-2000; 2000WO-US033873;
Publication Date: 21-JUN-2001; Priority: 15-DEC-1999;
99US-00464039; Assignee: (MILL-) MILLENNIUM PHARM INC; Cross
Reference: WPI; 2001-390244/41. P-PSDB; AAB84364; Patent Format:
Claim 2; Fig 3; 156pp; English.
COMMENT AAH25131-35 encode human alcohol dehydrogenase proteins, designated
21620, 33756, 21676, 21612 and 21615, respectively. Alcohol
dehydrogenase polynucleotides and polypeptides are useful for
treatment and diagnosis of disorders mediated by or related to
alcohol dehydrogenase. They can be used for treating disorders of
colon, brain, skin, heart, blood vessels, kidney, prostate,
skeletal muscle, ovary, testis and epididymis, spleen, lung, liver,
uterus and endometrium, T-cells, red cells, thymus, B cells, breast,
thyroid, pancreas, small intestine, reduced platelet number,
precursor T cell neoplasms, bone forming cells, and bone marrow
cells
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ss.DNA77626	TTGTGCCCCGTTGGGCACCTTGGCCTTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAA
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ss.P_AAH25131	1510 1520 1530 1540 1550 1560
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	1200 1210 1220 1230 1240 1250
ss.P_AAH25131	1570 1580 1590 1600 1610 1620
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	1260 1270 1280 1290 1300 1310
ss.P_AAH25131	1630 1640 1650 1660 1670 1680
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ss.DNA77626	CTCTGCCTGCCCCACTGCACCCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCCAGCCC
	1320 1330 1340 1350 1360 1370
ss.P_AAH25131	1690 1700 1710 1720 1730 1740
	AGTCTTGGCTTCTTGTCCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAG
ss.DNA77626	AGTCTTGGCTTCTTGTCCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAG
	1380 1390 1400 1410 1420 1430
ss.P_AAH25131	1750 1760 1770 1780 1790 1800
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	1440 1450 1460 1470 1480 1490
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	1500
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<first sequence: ss.AC003042 (length = 102818)
<second sequence: ss.DNA77626.rc (length = 1505)

<1495 matches in an overlap of 1505: 99.34 percent similarity
<gaps in first sequence: 0, gaps in second sequence: 6 (7410 bases)
<score: 4293 (match = 3, mismatch = 0, gap penalty = 8 + 1 per base)
<endgaps not penalized

ss.AC003042	10	20	30	40	50	60
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	CTCACCGCTGCCTGCTTCCCATATTTGTGGCCTGAACTGCGATGGCCTCTGGACACTGCA					
ss.AC003042	130	140	150	160	170	180
	GGACCTTAGCATTGTGAAGAAAGGCCTCTGGACCGAAAGTGGTTAGAGGAAGCGTGGGGG					
ss.AC003042	190	200	210	220	230	240
	CCTTGAGTGCCAGGAGACAAAGCAGGGGCTAGAGGTGAGGAAGAAGGAGAGATCCCCCTC					
ss.AC003042	250	260	270	280	290	300
	GTGCCTCCTTCTAAGAAACCCTGAGTGAGAAGACCATAACCGCGAGAAGGGAAGGTAGAA					
ss.AC003042	310	320	330	340	350	360
	CTCAGAGAGACTTGAGGCCATCAGAGCTTCTACCACGAGAGAGACCCACAGCCTAGAGAG					
ss.AC003042	370	380	390	400	410	420
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ss.AC003042	550	560	570	580	590	600
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	970	980	990	1000	1010	1020

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	8650 8660 8670 8680 8690 8700
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	8710 8720 8730 8740 8750 8760
ss.AC003042	ATCGTATGGTATATGAATTACATCTCAATAAAGCTGTTAACAAAACCTTTATTCTAAGTGA
	8770 8780 8790 8800 8810 8820
ss.AC003042	AAGAAGCCAGACCCAAAAGATCATCCAGAAAAGGCAAATCTATAGAGACAGAAAGTAGAT
	8830 8840 8850 8860 8870 8880
ss.AC003042	TGGTGGTTGCCTAGGGCTAGGGGACGGGGAGGGGACTGACTGTAAACTGACCCCTGGGAT
	8890 8900 8910 8920 8930 8940
ss.AC003042	CTTATTGGGATGACAGAAATGTTCTAGAACCGGGTTGTGGCAACAGTTGCACAATTCAAT
	8950 8960 8970 8980 8990 9000

ss.AC003042	ACCTTTACTAAAAACCATTGACTAGTATGCTTAAATGGGTGAATTTTATGATATGTAAA
ss.AC003042	<div>9010 9020 9030 9040 9050 9060</div> TTATACCTCTATAAAGTTGTTTTTAAAAACACAATGGGTGGATTCCACCCCCAGAGTTT
ss.AC003042	<div>9070 9080 9090 9100 9110 9120</div> CTGATTTCAGTAGGTCTGGGGTGGCTAGAGAATTTGCATGTTTAAACATGTCCCTGATGCTG
ss.AC003042	<div>9130 9140 9150 9160 9170 9180</div> CTGGCCAGGGAACACACTTGGAGAACCACTGGCCTATGGAGGTGAAAGGCCAAAGCCAA
ss.AC003042	<div>9190 9200 9210 9220 9230 9240</div> GAAGAGGGAAGTGGCCTGTTTAAAAAAATAAACCACCTTTGGGCACCAGCTCTCCACACC
ss.AC003042	<div>9250 9260 9270 9280 9290 9300</div> CACCCAGCACCCAATCCTCCAGCTAACCCGGGCAGGTAATAGGGTGAGGGGCTGCACTGG
ss.AC003042	<div>9310 9320 9330 9340 9350 9360</div> GCAGCAGGGAGCCGGCTGCTCTCCGTGCCTGGCAGACATTCCTCTGCATCAGACAGCAGC
ss.AC003042	<div>9370 9380 9390 9400 9410 9420</div> AGAGTTAATTTAAAGGCAGACTTCCAACATCAACCGAAATTGGCAGCATAAATAGGAAC
ss.AC003042	<div>9430 9440 9450 9460 9470 9480</div> TGCTGTTTATTTGCCACTTACCTCTGTCTTGTTCGCTTAAATACTGAGGGGAAACCAGA
ss.AC003042	<div>9490 9500 9510 9520 9530 9540</div> GCCATTAGGGTCAGAAGAAAATTACAAACACATAGGGTCTCTGTGGGCGGGTGAAAATGA
ss.AC003042	<div>9550 9560 9570 9580 9590 9600</div> TATTAGAGATGGGGGCGGCGGTGGGAGAAGCAAAAAAAAAATAGAGGAAGAAAGAGGGAG
ss.AC003042	<div>9610 9620 9630 9640 9650 9660</div> GATGGGGGAAAGAAAAAATGCCTTGTACCAAGAGTGCATGAAATAAAATAAAATTAAGTA
ss.AC003042	<div>9670 9680 9690 9700 9710 9720</div> AAGATCTGTTTGGCGGGTGGGGAATCTTCATCCAAGAAATATGGGTGGAGTTTGGGAGG
ss.AC003042	<div>9730 9740 9750 9760 9770 9780</div> AGGGATTTCTGGAGTTATTTTTAAAGCTAGATCAGGGAGAGTGTGAATTCTGATTTCTGT
ss.AC003042	<div>9790 9800 9810 9820 9830 9840</div> TTTCTGGCCTGATTAGCATGGTTGGGACTGATTCTCTTTCTCTCGGCCATCAGGAAACGA
ss.AC003042	<div>9850 9860 9870 9880 9890 9900</div> GTCCAGGGAAGGGACAAAAACCAAGCTAGCATCACTTCCACCATGAGGTATCTCCCCCA
ss.AC003042	<div>9910 9920 9930 9940 9950 9960</div> CCTCTGTGGTCTTAAAGCATCCCTCTTCTCTGGGGCTTCACATCCAGGGCAGCCACCTCTT
ss.AC003042	<div>9970 9980 9990 10000 10010 10020</div> CTCTACCTACCCCCGCCCCCTGGAAGAATTAATTGGAGGCAAGAGGAGCACCACATTTAT
ss.AC003042	<div>10030 10040 10050 10060 10070 10080</div> TACCTCCCCTCCTGCTCCACACTAAATCTTGTGGCAATGCTTCTAAAAGTCAATAAAATG
	<div>10090 10100 10110 10120 10130 10140</div>

ss.AC003042	AGAAGGAAGATGCGATAAAATTAAGGTGGAAAGTGCGATGGGGAGAGGAAATGGGAATCT
ss.AC003042	<div>10150 10160 10170 10180 10190 10200</div> TCTTTTAAATTTAGCTTTAATTTTAATTTTTTGTCACCTCTCCAAGCAGCCTTCGTGCTG
ss.AC003042	<div>10210 10220 10230 10240 10250 10260</div> CTGCAATGGAGAGGGAGCTGGGGGGAGGGGCTGGTTCTTTTAAAGGACTGGGTGAAGCCA
ss.AC003042	<div>10270 10280 10290 10300 10310 10320</div> CACACTGGCCTGGGTCTTGGTGGCAGGGGTCACGTCTTGGGGAGCCACAGCTGGGAGCC
ss.AC003042	<div>10330 10340 10350 10360 10370 10380</div> GGCATGGAGTGGAGGGGCTGCCTGTCAAATTCTACTGCACTCCCTTCTTTGGAGCTCCC
ss.AC003042	<div>10390 10400 10410 10420 10430 10440</div> AGAGAAAGCAGCTGATTATGCACTCCCTGAAAGCAGGGACTGTGTCTCGGCCTTCACTTT
ss.AC003042	<div>10450 10460 10470 10480 10490 10500</div> ACCCACAGTGCCTGGCACACAACAGCAGGAGTAGCAGTAATGATGATGATGGTGGTGATG
ss.AC003042	<div>10510 10520 10530 10540 10550 10560</div> ATGAGAGCAAATAGATACCAAGCACTTACTATGTTTCCAGCATTGTTCAAAGCACCTAC
ss.AC003042	<div>10570 10580 10590 10600 10610 10620</div> ACTTACTATTTCTTTCTTTCTTTCTTTCTTTTTTTTTTTTGAGACAGAGTCTTGCTCTG
ss.AC003042	<div>10630 10640 10650 10660 10670 10680</div> TCGCCCAGGCTAGAGTGCAGCAGCACGAACTCGGCTCACTGTAACCTCTGCCTCCCAGGT
ss.AC003042	<div>10690 10700 10710 10720 10730 10740</div> TCAAGCGATTCTCCTGCCTCAGCCTCCCATTAGCTGGGATTATAGGTGCTCACCACCAC
ss.AC003042	<div>10750 10760 10770 10780 10790 10800</div> AGCCCACCAATTTTGTATTTTGTAGTAGAGACGGGGTTTCACCATCTTAGCCAGGCTGGT
ss.AC003042	<div>10810 10820 10830 10840 10850 10860</div> CGCAAACCTCCTGACCTGGTGATCCACCCGCTCGGTCTCCCAAAGTGCTGGGATTATAGG
ss.AC003042	<div>10870 10880 10890 10900 10910 10920</div> CGTGAGCCACCATGTCCAGCCTACTATTTCAATTTACTTGTTACATTAACAATATTCATT
ss.AC003042	<div>10930 10940 10950 10960 10970 10980</div> AACTTGTTGCATTACAATAGACCCATTTTACAGACGAGGACATTGAAGACAGGAACTGA
ss.AC003042	<div>10990 11000 11010 11020 11030 11040</div> AGCACTTTGCCCATGGTCACAGAGCCAGTAGGTCAAATAGGCAGTGGATACTTCTCATGT
ss.AC003042	<div>11050 11060 11070 11080 11090 11100</div> ATCGAGAAATAGACAGTGGATACTTCTCATGTATCGAGAAATAGACAGTGGATACTTCTC
ss.AC003042	<div>11110 11120 11130 11140 11150 11160</div> ATGTATCGAGTGGATTAATAAACGAATGGATAAAAATTGCATAAGAGGGGTGGGGTGGAA
ss.AC003042	<div>11170 11180 11190 11200 11210 11220</div> GAAAAAATGGCATAAGAATGCCGACAAAGTGACAGCTATGTAGGTACCAGTGATTCTAC
	<div>11230 11240 11250 11260 11270 11280</div>

ss.AC003042	GGTGCCCCATCTGCCATCAGTCCATGAATGCAGAGGGGTGCTTAGCAATGCTGAGATAGG
ss.AC003042	11290 11300 11310 11320 11330 11340 GGAAGGTGGGCTTAGTAGGAGGCAGTCAGAGTCTTCCTGGTATTGGTGGGCAAGCCCTTG
ss.AC003042	11350 11360 11370 11380 11390 11400 AAGTTAGACCATCCTTTCCTGTCATGTGATTTCTTTCCCATTTTTAGGAAAGATGAAATC
ss.AC003042	11410 11420 11430 11440 11450 11460 ACACACACTCCCCATCTCCACCCCCAAAACCAGAAGATGTTCTCTCCAGAGTGGCTCAA
ss.AC003042	11470 11480 11490 11500 11510 11520 CCATGACATAGAGGGTCTGTGGCTCCAGCTGTGACCCCTTCCCCAAGAACAGGGCCCTGA
ss.AC003042	11530 11540 11550 11560 11570 11580 GGCAGCAGCAGCACTGACCCTCCTTCACCCAGCACTAGCCAGGTGTCCTGAACGTCTGT
ss.AC003042	11590 11600 11610 11620 11630 11640 AGCCAGACCCAGCTTGGCCTATCAGAGAAGTGCAGATCTGGGAGCTCTCAGGATACTTAG
ss.AC003042	11650 11660 11670 11680 11690 11700 AGATTGCCGAGTGCAGCCCTGCAGTTTACATGCAAGTCTCGGGCAAGAGGACAGGGCTTC
ss.AC003042	11710 11720 11730 11740 11750 11760 CCTTGGGTCTCACAGGTGGCCAGTGGGAAGGCTAGGTCTCTTGGCCTCTCTTCTGTAACC
ss.AC003042	11770 11780 11790 11800 11810 11820 CTGAGGTCTGTCCCATTCTTTCTACCTGATGGGAGCTCCATCTTCAGTATTTTTTGA
ss.AC003042	11830 11840 11850 11860 11870 11880 TCATACGTGGGCTCGTATCTCAGTCCTTGATGACAGTCCACCAGGAGGTGAGCAAGAGAT
ss.AC003042	11890 11900 11910 11920 11930 11940 AGTTGCTGCTTCCTCTGCATACAGATGGGGAAGTCTGAGGCTCAGAAGGCTTCAAAGATGT
ss.AC003042	11950 11960 11970 11980 11990 12000 TTCTAGGACCATGTACTAACACCGGTATCAGGCTCTAACCATGCCAGTGAAGGATTCTG
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ss.AC003042	12070 12080 12090 12100 12110 12120 ATCAAGCTCAGGTTCTGAAGCAGTCCTGCCCCCTTCTCTGCCCCACTTCTGACCACAAG
ss.AC003042	12130 12140 12150 12160 12170 12180 GACCCACCAGGTAAACCCGCCCCACCCAGCATCACCTTCCCGAAGACCTTGCAGCGTTCC
ss.AC003042	12190 12200 12210 12220 12230 12240 TAACTGGGGGAGGCAAGAAAGGATGGACTTCTTTCCTAACAGAGTCCCCATTGCCCAA
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ss.AC003042	12310 12320 12330 12340 12350 12360 CACATGAAGTATCTGTAAGTTAGAAAAAAAATGCAAGTTACCAAATGCCATGCAGAATA
	12370 12380 12390 12400 12410 12420

ss.AC003042	CTATCCTAATTATGTTTTGTTTCAAATACAGTTCATAGGCCGGACACAGCAGCTCACGCC
ss.AC003042	12430 12440 12450 12460 12470 12480 TGTAATCCCAGCACCTGGGGAGGCCGGGACGGGAGGAGTTCTTGAGCCTAGGAGTTTGAG
ss.AC003042	12490 12500 12510 12520 12530 12540 ACCAGCCTGGGCAACATAGGAAGAACCATCTCTACAAAAAATCAAAGAATCAGCCGGGT
ss.AC003042	12550 12560 12570 12580 12590 12600 GTGGTGGTGTGTGTCTGTGGTCCCAGATACTCAGGAGGCTGAGGTGGGAGGATTGATTGA
ss.AC003042	12610 12620 12630 12640 12650 12660 GCCTGGGAGGTTGGGGCTGCAAGGAGCCGTGATCTTGCCACTGCACTCCAGCCTGGGTAA
ss.AC003042	12670 12680 12690 12700 12710 12720 CAGAATGAGACCCTGTGTAAATAAATAAATAAATACTGTTTATGCCTATATTTATGTAT
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ss.AC003042	12790 12800 12810 12820 12830 12840 TGTTTACAGTGTTTACAAAATGTTTACAGTGTTTACAAAATGTTTACAGTGGTTTCTGTT
ss.AC003042	12850 12860 12870 12880 12890 12900 TTCTTCCTTATATATTTGTATATTTTCCAGAGTTTCTGCTGTGAATGTGTCCTTTCACAA
ss.AC003042	12910 12920 12930 12940 12950 12960 CGGTATAAAAGGAAATTATTATTATTATCTTTTTTTTCAGAGATGGGGTCTGGCTCTGTCTG
ss.AC003042	12970 12980 12990 13000 13010 13020 CCTAGGCTGGAGTGCAGTGGCGTTATCATAGCTCACTGCAACCTCTACCTCCTGAGCTCG
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ss.AC003042	13150 13160 13170 13180 13190 13200 ATACAGACCCCCTTCTAGCTTGCTGGTTCTGCTGCCTTGTAAGCAGCAGCCAGGAACGAT
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ss.AC003042	13270 13280 13290 13300 13310 13320 CAGTGACTGCTGTTTCATCATAACCAGGACAATTAACCATCCCCTTATTATTACACGTCA
ss.AC003042	13330 13340 13350 13360 13370 13380 TGATTACTAATCACCTTATTAATAATCCATGCTTTGCGAAACCAGGAGGCAGCTTGGCTC
ss.AC003042	13390 13400 13410 13420 13430 13440 AGATGCTTGGAACCTCCACAGGAATCCAATCCTGACCCAGGCGAGTCCCTTCCTGCTCTG
ss.AC003042	13450 13460 13470 13480 13490 13500 TGCCTTCACCTCCCCCTGGATCAGGAGGATCTGCTGCTTCCTCATCCCTTCAGTGACCAG
	13510 13520 13530 13540 13550 13560

ss.AC003042	GGCCCTCTGCTTCCCTCCTCTGCCAGCTCTTAGAGCCCCACATCCCCGGAAGGCCATCTG
ss.AC003042	13570 13580 13590 13600 13610 13620 AATTCCTAACTCCACTCGCCACCTGCGCCACCAACCTCCCTTTACACTGGAAGTGAACA
ss.AC003042	13630 13640 13650 13660 13670 13680 AGGGTCTCCTCCTGTCTTTGATCCTTTTTCCCAAATTACTCACTTTGTTTATAAAATGTA
ss.AC003042	13690 13700 13710 13720 13730 13740 CGCTTTCCACCAAATAGAGATGCTATGGCTAAAGACTGAACTTTATGGTTATAACATTTA
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ss.AC003042	13810 13820 13830 13840 13850 13860 CCAGTTAATGATAACATTGGCCATTTGACTAATATTAAATTCCCTGGCTAATGTTTGGTG
ss.AC003042	13870 13880 13890 13900 13910 13920 CAGATTTATACTACGGGTCTTTTACCCCCCAGATTTTGTGGTGGTGGTGGCTCTGAGTA
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ss.AC003042	13990 14000 14010 14020 14030 14040 CATGGAGAATTTACAGTGCATCAATGTGCCAGCCCCTAAAGGGGGCATTGTAGCTTCTTC
ss.AC003042	14050 14060 14070 14080 14090 14100 TGGCTGGAGGTGAATCCAAGGCAGCCCCAAGAGGTGGCTGCCACCCATCCCTGCTTTGAT
ss.AC003042	14110 14120 14130 14140 14150 14160 CATGTTCTGGGTGAGTACGCTAGGTACTGACCACCACCCAGACCCTGTTGAGACAAAGA
ss.AC003042	14170 14180 14190 14200 14210 14220 GTCCTGGTTTCCATTCCCTGAACGTACTCGTGGAACATACAGGGGATGAAGATAACAACAG
ss.AC003042	14230 14240 14250 14260 14270 14280 TAATTTGAACAAAATACAGCAGTTGCATTTATTATAGCAAGAAATTAGACACCTCACACA
ss.AC003042	14290 14300 14310 14320 14330 14340 TATCCAACGATGAGGGAGTGACCAAACAAAATGATCCATCAACATGATGGAATGCCATGT
ss.AC003042	14350 14360 14370 14380 14390 14400 GGCCATTAAAACGACAAGACAGGAGGCCCTGCCACCCCGAAAATGACCGTGTGAGTCGAT
ss.AC003042	14410 14420 14430 14440 14450 14460 GTTAGGTAAAAGCAGGAAACCCAGTGGAAGGGCAGTGACACTGGAGACATATATCCAGG
ss.AC003042	14470 14480 14490 14500 14510 14520 GGAAACAGCTCTGCACCAGCACAGGGGGAACAGGTTCAAACCTAGGCTCAGCTGTTAAC
ss.AC003042	14530 14540 14550 14560 14570 14580 ATGCCTTAGTTGCCCCATTTGTAAAAGAAAATCAACACCCCTGGGCCAGTGTTGTGGGA
ss.AC003042	14590 14600 14610 14620 14630 14640 GGGCTACAGCAGGTGCGAGATGTGAAAGCCAGTTCATAGCACTCAGGATCTTTCAGACAC
	14650 14660 14670 14680 14690 14700

ss.AC003042	CTGGTAACAAAAATGCCCGAAAAATCCAGAAAGAACTGATCAGAATGGAAACATGTACAA
ss.AC003042	14710 14720 14730 14740 14750 14760 GTTCTTTCGCTCCTTTTTGGAGTAAGTCCATGTAATAAAAAAGACAGGAAATGGTTTGGG
ss.AC003042	14770 14780 14790 14800 14810 14820 AATAGGGGCTCTAGAGCTTTGAAGATTCTCCATGGAGGATGTAGTTGGTGGCCCATGGAG
ss.AC003042	14830 14840 14850 14860 14870 14880 GCTGGCTGGGCTCTAGAAGAATGGGGGAGAGAGAAAATGTGGGCTCCCCACCCACCCTAG
ss.AC003042	14890 14900 14910 14920 14930 14940 GGCCCCAAAGAGGACCAAAGCCACATCTAAGTAACTGGGGGCTGAGAAATCCCAAGCTCA
ss.AC003042	14950 14960 14970 14980 14990 15000 GTCTACAGTGAGAAGGGACAAACATCACCCCCAGCGCGCAGCTCCCAGGAAGCACAGTGG
ss.AC003042	15010 15020 15030 15040 15050 15060 AGCCCGGAGAGTCACCTGGAATTCATCTCCTTCAGAGACCATGAGAGAGACAGAGGAGGA
ss.AC003042	15070 15080 15090 15100 15110 15120 GAGAATCAGAGGCAGAGAGATAGAAGGAGGCACAGCGGAATCAGCCAGGGAACAGGCCT
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ss.AC003042	15190 15200 15210 15220 15230 15240 CAGCCTGCTCCAGGAGCAAGAAAAATAAAATAAGCAGCTCTGACAGCTGGCTGCCTACGC
ss.AC003042	15250 15260 15270 15280 15290 15300 CTCCTCCCTCTCCTCCCCTCCTCTCTCCCCTCCTCCTCCTCCTCTTTCTCTGCTCT
ss.AC003042	15310 15320 15330 15340 15350 15360 TTCCTCCTCTTCTCCTCCCCTTCTCTTCTTCTCCTCCTCCTCCTCTCTCTCTTTGT
ss.AC003042	15370 15380 15390 15400 15410 15420 CGTCTTCTTCTCTTCTCTCGTCCCCTCCTCCCTCTCCTCTCTCCCTCCTTCTCTCCAT
ss.AC003042	15430 15440 15450 15460 15470 15480 CCCCCTGCCCAAACACCATCTCCTGGTATCTGTTCTTCTGAAGGAAGAGGGTGTGAGCCGG
ss.AC003042	15490 15500 15510 15520 15530 15540 ATGTAATGCAAATACTCTACAGGAATGTTTCTGGCAGGGAGCAGAATCCTCTTCCCTCAC
ss.AC003042	15550 15560 15570 15580 15590 15600 GGACCCAAGGATGAAACAGGGCCCCAGACGCCAAGCTGAGGCTGCTCCTCCCTTTCTCTG
ss.AC003042	15610 15620 15630 15640 15650 15660 AAGACAGTCTGGGGACCTCAGATAGGGGGCTCCCCCTCCAGTCTTCTCTCCAACACCACCT
ss.AC003042	15670 15680 15690 15700 15710 15720 TCTTCCTTTGAGGAGTGGGAGTGGGGTTAAGGAGGCAAAGTGACGACCTGAGGGAGAAGG
ss.AC003042	15730 15740 15750 15760 15770 15780 GGAGACGGGAGGGGCTTCTCTGGGGACATTCCCCTCAGGGTTTCTGAAGCCTGTGATC
	15790 15800 15810 15820 15830 15840

ss.AC003042	CCCGCGGTGAAGGAGAAAGGAGGCAAGCCACCCACAGGGAGCAAAGCAAATCGGGGATTC
ss.AC003042	15850 15860 15870 15880 15890 15900 AAGGGAACAGTTTTGTAATTATCCAAATAATTCAGCCTCCTACTCTTTTCCCAATATATC
ss.AC003042	15910 15920 15930 15940 15950 15960 CCGCTTTTGTTTTTAATAATCCAGGAATTGGGAACAACGCCCTTTCCGTTTTACCGCACTT
ss.AC003042	15970 15980 15990 16000 16010 16020 ACCCTTTGCTCTAGGAAAGCAGCCTATTTCACAGCCATTTTACGGCTGTGTGCCAGCTTT
ss.AC003042	16030 16040 16050 16060 16070 16080 CTCACTGAAGGCCTTTGCCCATGCCATTCTCCACCGCATCCCCTTCCCTTCTCCACCT
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ss.AC003042	16150 16160 16170 16180 16190 16200 TGGAATCTCCAGCCAGAAAAGCTCTTTTCGTCTCTGCTGTCCTGGAAAGGACATTTACT
ss.AC003042	16210 16220 16230 16240 16250 16260 CTGGGATTTTCAGCTCACACCATATCTCCAACTGGATGGCATCCTCTCCATGATCCTTTC
ss.AC003042	16270 16280 16290 16300 16310 16320 ACCCAATCAATCAATCAATGAGCTGAGAAAGAATTGGGGTGGGGAGATGGCAGTGGGGGG
ss.AC003042	16330 16340 16350 16360 16370 16380 GAGCACAAAATTGCCCAAATCCTCGTTAACTGAGACTTGGACAGGCTTGGACTCACAGTT
ss.AC003042	16390 16400 16410 16420 16430 16440 GGAGGCACCTGACACAGATTATCCCATGAAGGTTGCATGCCCCACCCACAGGCTAGGTCC
ss.AC003042	16450 16460 16470 16480 16490 16500 TCTTACCATCCCATCTTGCCCCAGACACCCCCAGCTAGTGAGGATTTGAACCCAGCCTGG
ss.AC003042	16510 16520 16530 16540 16550 16560 CCAAGTCCAACACCCACTCTCTTCCACTCCACCACACTGCTTCTACTGCCCCCTTCTCT
ss.AC003042	16570 16580 16590 16600 16610 16620 GGGGAAGAGAGGTTAGAAATGGGTATATGGCCGGGAGCTGGCTCTCTGGCTCTTTGCTT
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ss.AC003042	16690 16700 16710 16720 16730 16740 GAGATGGGGCTGGGGAGCCCTGGGCACTAACAAGTATTCATGCAGGTAAGCAGGTACCAG
ss.AC003042	16750 16760 16770 16780 16790 16800 GAGCCAGGAGGGGCACATCAAAAACCTCTAGAACAGGCCAGGTGTGGAGCTGTAATCCCA
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ss.AC003042	16870 16880 16890 16900 16910 16920 CCAACATAGCAAACTCCGTCTCTACTAAAAACAAAAATTACCCAGGTGTGGTTATTT
	16930 16940 16950 16960 16970 16980

ss.AC003042	TTCCCTGGGTTGTTCTGTAGCTTGGCAGCAGGAATTAAGACTAACAGGAAAGGGGTCAGT
ss.AC003042	16990 17000 17010 17020 17030 17040 TGTGGAGAGGTGCATGGAGAAGAGGATGTTGGAAGAGGGGAGCAAGGACCCCCAACCTCT
ss.AC003042	17050 17060 17070 17080 17090 17100 GCAGACAACCTTGTCCAGCCAGAGTTGAGGTAGGGGGAAGGGTTGATCCCATCTCCATC
ss.AC003042	17110 17120 17130 17140 17150 17160 TCTGAGAAAGATTTATTTCTTCACTTCCCTAAGGTCTTTGGAGAAATGCTGCAACTCTCA
ss.AC003042	17170 17180 17190 17200 17210 17220 GCCTGGCCCTCATCTCCACACCTCTGCCAGCACCTCAGTTCCAGCCCCAGGGCTCCAGGG
ss.AC003042	17230 17240 17250 17260 17270 17280 ACAGACTCCTAACATGAACTGCCAGGATACCATATATCCATCCATCTGACAGCTTACCTG
ss.AC003042	17290 17300 17310 17320 17330 17340 AGCTCAGACGGCCTGCAAAGTGGCAGGACAGGAGGGATGCCCCGCGTTTGGTGTGCTGAG
ss.AC003042	17350 17360 17370 17380 17390 17400 TGCCTTTGTGTGTGTGATCTCATTCAAGGTTCCCAACTCTGAAAGCAGACATGATTAGCC
ss.AC003042	17410 17420 17430 17440 17450 17460 CCTTTCACAAAAGGAAGCAGAGGTCTTAGTGACTTGCCCAAGGTCACATGCCTAAACAGG
ss.AC003042	17470 17480 17490 17500 17510 17520 GACACAAACCCGCAGGAAAGATGGAGCACAAATGCTGGGGTCTCTGATAGTGGTGCACAC
ss.AC003042	17530 17540 17550 17560 17570 17580 ATGCACACATGTGCACAAATACATGCACACATGTGTACCCCAAATCATTTAAATGGACCA
ss.AC003042	17590 17600 17610 17620 17630 17640 TTCCCCCTCTGTGTGTGATGTAGTTTACAGATCCCCGTGTGCTCCCATGCATTATCTCAGTT
ss.AC003042	17650 17660 17670 17680 17690 17700 GGTTTAACAACAGGGTCCCGTGGTAACAGGCAGGGCAGATGTCATGAACCCATTTCTCAG
ss.AC003042	17710 17720 17730 17740 17750 17760 ATAAGGAACCCAAGGTTCAAAGAGGGTGAGCAATCTGCTCAAGGTCACAGTCTCCAGAGC
ss.AC003042	17770 17780 17790 17800 17810 17820 TTTGATCACAATAATACTGACAACTCCACCTCCGTTTACGTTTGTAAATGCAGGAGCT
ss.AC003042	17830 17840 17850 17860 17870 17880 GGGTGCTAAGCACCTTCCATGCATCTAACATTCATGGTCATCCCGTGGGGGAGACATTGT
ss.AC003042	17890 17900 17910 17920 17930 17940 TATTATTCCCATCTTACAGATGATGAACTGGGACTTAGAGGTGTTAGATGATATGGGGC
ss.AC003042	17950 17960 17970 17980 17990 18000 AGCCACATAGAGTTAAGCCCCAGCCAGCCTGATTTTACTCCAGGAACTCGCCCAGGAC
ss.AC003042	18010 18020 18030 18040 18050 18060 GGGAAGCTTATTCACCTGGGCCCCCGAGTCCCAGCACCTAGACCAGTGCCTAGCCCACAT
	18070 18080 18090 18100 18110 18120

ss.AC003042	GAGGTTCTCACTGAGCGTTTGTGGAACATTTGTTAACCAAATAAATCTGCCCCCAATGCC
ss.AC003042	18130 18140 18150 18160 18170 18180 CTTACCCTCAACTTCCTCCTCCCAGACCTTTCCCTGCCCATCTCCTAACTCCTCGAATGT
ss.AC003042	18190 18200 18210 18220 18230 18240 CTCTAGCGAACCATTTCGAGACCTCTCCCCCAGGAGTCGAGGGTTACAGACCCCCCTCAGTC
ss.AC003042	18250 18260 18270 18280 18290 18300 CCTGCAATGGGACCGGGAAGTCAATTACACCTCACTCTCCTATCCCTATTAGCATTCA
ss.AC003042	18310 18320 18330 18340 18350 18360 GGGATTTGTAGTTTGTCTTAAGGTTCTCCCTTGCCCTCAGTTTCCGCCCCCTGGCACCAGA
ss.AC003042	18370 18380 18390 18400 18410 18420 TGTGAGGGAAGTAGGCAAGCAGACTGCTGGAGAAGAGGTCCCCTGAAAAGCCCCACCCCTC
ss.AC003042	18430 18440 18450 18460 18470 18480 TGCTTTCTTGTCCCACAAGCAAGTGCTGGGGATTTCTTTCTTCTCTCTAGATCCCGCA
ss.AC003042	18490 18500 18510 18520 18530 18540 GAGCCCCAGACAACGGACGAGACAAAGAGCGGGCAAGCGGAGCAGTCAGGCCCAGCTCCA
ss.AC003042	18550 18560 18570 18580 18590 18600 AGGCATGCATTTCCAAACAGGGAAAATGTGGACATCTGAGGACGGGGTCTCTCAAGGATA
ss.AC003042	18610 18620 18630 18640 18650 18660 CTCCCCCAAGTACAAGTTTGGAGGCCCTTTTGGAACTGCCAATTCCAGCTGCCTCC
ss.AC003042	18670 18680 18690 18700 18710 18720 ACCCCCAGGCACCAATCACTCAACAGCACCGAGTGTTTACTGGGCCTGCAGGCAGGGAAA
ss.AC003042	18730 18740 18750 18760 18770 18780 TAATGCAAGATGCCACTTCTGCAAACCTGGCAGGACAGGAGGGATGCCCTGCATTTGGTGT
ss.AC003042	18790 18800 18810 18820 18830 18840 GCTGAGTGCCTTTGTGTGCATGATCTCATTCAAGGTTCCCACTCTGAAAGCAGAAACGA
ss.AC003042	18850 18860 18870 18880 18890 18900 TTAGGAAGCAGAGGTCTTAGTGGCTTGCCCAAGGTCACATGCCTAAACAGGGACACAAAC
ss.AC003042	18910 18920 18930 18940 18950 18960 CTGAGGCCTTTAGGTCCTGTGCCTGGGTCTTGCTCTCCAAGCAAAGCTGATCCTTCAGTC
ss.AC003042	18970 18980 18990 19000 19010 19020 ACATCTGCCAAGGCTTCCTTTCTACCAGCTGCAGGCATTGTAAACAAGCCCCCATGCCT
ss.AC003042	19030 19040 19050 19060 19070 19080 CTTACCCAGCCCCCTTGTTCCAAGGGCAAGGCAGATGGCCAAACCACTCCTGGGAGACCCC
ss.AC003042	19090 19100 19110 19120 19130 19140 AGGTCTACAGCCCTAGGCTTTAGTGGTCAATGAGAGGACAACCTTCCCCAGGCCCTTAAC
ss.AC003042	19150 19160 19170 19180 19190 19200 TGGCTGAGGGGTGCCGGGCTGCCCCACCAGGGCCTGCTGATGTGCCCCCCCCCACCCCAT
	19210 19220 19230 19240 19250 19260

ss.AC003042	CCCTCCCCTCCAGCTGCCCTCTGGTCCCTCTGCTCCTCCCCTGCCCCGCTTTCAGCCCC
ss.AC003042	19270 19280 19290 19300 19310 19320 GACCCAAGAATGACCAGGAGTCACGGGTGGAGGAGCAGAGTTCTGGTCCCCAGCCTGGC
ss.AC003042	19330 19340 19350 19360 19370 19380 TTCTGACATCTCCGGCGCCCCTTGGCCTACCCTAGGTGCGGGGTGTCAGGTCCAGTGAGAC
ss.AC003042	19390 19400 19410 19420 19430 19440 CAGCCTCCCCTCAAAGCCATCCAGCCCTGCCCTCTGGCCACTAGGCAGCCACATGCTCAG
ss.AC003042	19450 19460 19470 19480 19490 19500 AGGATTGTCCAATGTCAGAGCGCCATCTAGTGTGAATGATGGGCACTGCACCCCTGCCTG
ss.AC003042	19510 19520 19530 19540 19550 19560 CCGCCGAGCTCACCCACTTGGCAGGACCTCTCATGGGGGTGGCCGGGTGCAGAAAGGGA
ss.AC003042	19570 19580 19590 19600 19610 19620 GACGCCCTCAGACTCACAGAGGGCGCCAAATCTAGACTTCTGACATAGTGTCCAGATGAC
ss.AC003042	19630 19640 19650 19660 19670 19680 ACTTTTCCTCCAGTCATGGGAGAGACCCTAGAATCCAGCGAGGGCAGTCCCCTTGCACTG
ss.AC003042	19690 19700 19710 19720 19730 19740 TGAGAATGTAGGATGACACTGCCTGGAGGGCCCTGTCACTATTTGAAAGGCTTAAATGA
ss.AC003042	19750 19760 19770 19780 19790 19800 CCTTTTGAAGAGCCTAATCTCTTTGCACTATTTTGTGTGCACTGGTGAAAAGTAACTTT
ss.AC003042	19810 19820 19830 19840 19850 19860 CTAAATCGGCCATAATTTGGGTGACCTCTTTTGGCAAATCTTAAACAAGAGCCTCAAAG
ss.AC003042	19870 19880 19890 19900 19910 19920 AACAGGGGCTAAGGCATTGTCAGACCCAGAAGAGGCCCCACCGTGTGCATGAAGCCTGCA
ss.AC003042	19930 19940 19950 19960 19970 19980 CTCCATGCCTTGCTCAATCTGTTTCATGGGTCTCTCTCTCTCTCTTTCTCTCTCTCACTC
ss.AC003042	19990 20000 20010 20020 20030 20040 ACTCTCCTCTCTCTCTCTCTCCATCCTTGATCAGCCTGATGGAGTCCAAAGACCACTAAG
ss.AC003042	20050 20060 20070 20080 20090 20100 TCCAGGCAGGGAGGTGAGGCTGATCTGGGTTTGAATCCTGGCTCTACATGAGCTGTGTAA
ss.AC003042	20110 20120 20130 20140 20150 20160 CCTTGAGAAATTCACATTGAAATTTCTAAGCCTTACTTTCCCCATCTGTAAAATGGGGTTG
ss.AC003042	20170 20180 20190 20200 20210 20220 TGATGAGCATTGTGTGAAATAACAAGTTTGAAGCACTCAGCAAAGTGTGAGCTGCTTATC
ss.AC003042	20230 20240 20250 20260 20270 20280 AGAGGCTCAGTAACTGCCAGTCTCATCCTCCTCATCTCTCTCAGGGCCTCCATCGCTGAG
ss.AC003042	20290 20300 20310 20320 20330 20340 TCAGTGTCTCTCTGGGGGTCCGCTTCTGCAGCACCTGGCACAGGGTCTCCATCATTCTCT
	20350 20360 20370 20380 20390 20400

ss.AC003042	TGGTCTCGGAGCACTGGCCCACTGCACCTTGCATCTCACACTGCATCCTGCATGTCCAT
ss.AC003042	20410 20420 20430 20440 20450 20460 TTTCCATGGTTATATCCATCTACTCCCACCCACCTGATCCATGACTCGGAGCTTCCTAGG
ss.AC003042	20470 20480 20490 20500 20510 20520 GTCTCTGTTTCTCTCTTCTTCCCCTCCGGAAGCCCAGCCCAGTTTTGAGCCCATGGCAAG
ss.AC003042	20530 20540 20550 20560 20570 20580 TGTGTATCTGCCTGCAGCTGAACTGAATGTTCCCAGGCACAGTTAGAGAAGCCTGTTCTG
ss.AC003042	20590 20600 20610 20620 20630 20640 CAATCCAGGAGCTGAACCAACACATGTTTCTAGCCCTGCCAAAACATACATTTTGGCCAG
ss.AC003042	20650 20660 20670 20680 20690 20700 GTGCAGTGGCTCGTGCCTATAATCCTAGCACTTTGAGAGGCCAAGGCCAGAGGATTGCTT
ss.AC003042	20710 20720 20730 20740 20750 20760 GAGGCCAGGAGTTTGAGACCAGCCTGAGCAACATAGGGGGACCCAGACTCAAAATATATA
ss.AC003042	20770 20780 20790 20800 20810 20820 CATACACATTTTCTCTCTCAGTAAAATGGTATTGAAGCTCCTGACTTGACACAATTGTTAA
ss.AC003042	20830 20840 20850 20860 20870 20880 AGGGATTAGAGAGAGGGCATTTCGAAAGGCATTATATAAAGAGTATAAAACACAGTAGGCC
ss.AC003042	20890 20900 20910 20920 20930 20940 CTCAAAAATAGAACTTATTACTATAACAGCTAGGGAGGCCCTGTTGATGTTCAAAAATA
ss.AC003042	20950 20960 20970 20980 20990 21000 TGTCCAGGCTGGGCGCAGTGGCTCACACCTGTAATCCCAACACTTTGAGAGGCTGAGGTG
ss.AC003042	21010 21020 21030 21040 21050 21060 GGCAGATCACTTGAGGTCAGGATTTCAAGACCAGCCTGGCCAACATGGCGATACCCTATC
ss.AC003042	21070 21080 21090 21100 21110 21120 TCTACTAAAAATACAAAAAATCAGCTGGGCGTGGTGGCGTGTGCCTGTAATCCCAGCTA
ss.AC003042	21130 21140 21150 21160 21170 21180 CTCGGGAGGCTGAGGCAGGAGAATTGCTTGAATCCAGGAGGCGCAGGTTGCGTGAGCCAA
ss.AC003042	21190 21200 21210 21220 21230 21240 GATTGCACCACTGCACTCCAGCTTCAGTGACCAAGCTGGTCTCAAAAAAAAAAAAAAAAAA
ss.AC003042	21250 21260 21270 21280 21290 21300 AAAAGAAAACAGTGTCCAAAGAAGACAGGATGAGTAGTATAATCTCAATTGTACAACCTC
ss.AC003042	21310 21320 21330 21340 21350 21360 AAAAGAGACACCAGGGCAAGGAGGCAGAAGGCAAGAAGGGAATGGTGGGACACGATTAAT
ss.AC003042	21370 21380 21390 21400 21410 21420 ATTGGCCAAGATTATAACCCAGTCAGGGTCTCGTCAACAATTTAAGAGTAAGGCATCCCA
ss.AC003042	21430 21440 21450 21460 21470 21480 CAGGCCAGGGGTAACCAGGTGGAGAGAATCCTCTTTCCACCGGATAGGGATGGGAAACAG
	21490 21500 21510 21520 21530 21540

ss.AC003042	GCAAAGCGGGATGGGGAATGAGAGGCGAACAGCCTCTTTATTAACACAATTATTTTATTT
ss.AC003042	21550 21560 21570 21580 21590 21600 GCCGAAAGGTAATCATCTAAGTGAGGTCAACGGCGGCTGGCACAGGACTGGCCCTGCAG
ss.AC003042	21610 21620 21630 21640 21650 21660 GCGGCTGGGCCACGTTGCCATGGTGACGGAGCCCGCTCACTTCCAGCAGCTGCAAGGGCT
ss.AC003042	21670 21680 21690 21700 21710 21720 GGAGAATCCTGAGGAAGGAGACCCAGGTCTCTTTTCTTTCCCCCAAAGGGGCTGAAGG
ss.AC003042	21730 21740 21750 21760 21770 21780 AGACCTGCAGGTGTTTGCATTCCCCGTCCCAGCCCCAAGAGACAGACTAAGAGCCCTG
ss.AC003042	21790 21800 21810 21820 21830 21840 GGGAAATGTCCCAGCCCAGGTTGCGAGGGGGTCCATCCTGGAGCACAGGGGTCTCTGCGG
ss.AC003042	21850 21860 21870 21880 21890 21900 GCATCATCTCATTCTGTCCTACAATAACCCTGTGAGGAAGAGGCTACGCATCACCTGACC
ss.AC003042	21910 21920 21930 21940 21950 21960 ATTTACAGAAAGCTGTGGCTCAGACTGTCCGCAGATGCGCAGCATGTGGGGATTTGGGG
ss.AC003042	21970 21980 21990 22000 22010 22020 GCTGGGGTCTGAGGCCTGGGGCACCATTACATTGCTCAGAGTCAGGGCTGTGACAAT
ss.AC003042	22030 22040 22050 22060 22070 22080 GACAGAATTAAACCTACATCTTGAATAATCAGAAAACTGATGTGGAGAAAAACACACTC
ss.AC003042	22090 22100 22110 22120 22130 22140 ACCCGGCAGTCAGAAAGGCCTGGGTTGAGTGTCAACCCTTCCCCTTACAGGCCACGTCA
ss.AC003042	22150 22160 22170 22180 22190 22200 CCCTCAGCAAATTTGCTCTAAGCCTTAGTCTGTCCAGAGCATTCTGCACCTGTGACTTTC
ss.AC003042	22210 22220 22230 22240 22250 22260 CAGTCTCTGAAAGACAGAGCCATGATCAAGGTGTGCTTCCCCATCTGTAAATGAGCCAA
ss.AC003042	22270 22280 22290 22300 22310 22320 CTCAGTTGGGTGCAGTAGCTCACACCTCTAATCCCAGCACTTTGGGAGGCTGAGGCAGGC
ss.AC003042	22330 22340 22350 22360 22370 22380 GGATCACTTGAGGTGAGGATTCAGATCAGCCTGTCAACATGGTGAAACCCATCTCTAC
ss.AC003042	22390 22400 22410 22420 22430 22440 TGAAAATACAAAATTAGCCAGGTGTGGTAGTGGGCGCCTGTAATCACAGCTAGTCAGGA
ss.AC003042	22450 22460 22470 22480 22490 22500 GGCTGAGGCAAGAGAATCACCTGAACACGGGAGGTGGAGTTTGAGTGAGCCGAGATCAC
ss.AC003042	22510 22520 22530 22540 22550 22560 GCCACTGCACTCCAGCCTGGCAACAGAGGTAGACTCCATCTCAAACAAACAAAAAAGC
ss.AC003042	22570 22580 22590 22600 22610 22620 CACTCAACCCTGCCCTGGGGACCCAGAACGTCAACAGTGAAGTGGGAACTCACGCACTAC
	22630 22640 22650 22660 22670 22680

ss.AC003042	ACAAACAAGAGCAGCTGGCTCTGTCTTTTCACCCAAATCTTCAGGGATGGCAGCTCTGCA					
ss.AC003042	22690	22700	22710	22720	22730	22740
	GAAAAGGGACACAACATGCACTGTCCCCAAGTCCTCCAGCCCTGAAGTCCAGCGGTGAGG					
ss.AC003042	22750	22760	22770	22780	22790	22800
	ATGCCAGGCTGGAAGTCCAGGGGACAGCATAGCAGAGGCAGGATGGGTCCGGGGGCGGGG					
ss.AC003042	22810	22820	22830	22840	22850	22860
	AGGGGAAACGCAGCCAATCCTGGGGCCATTTTGCTTGTGCCCCGAGTGTCTGTGCGCCCTC					
ss.AC003042	22870	22880	22890	22900	22910	22920
	TGGTGGACGCACCTGACACAGACGCAAGGAACAGCTGTGCAACCAGAGGGAATTCAGGTT					
ss.AC003042	22930	22940	22950	22960	22970	22980
	GGGGGGTCGGCGGGGGGCATGGCTGGAGGAAGTAGGAGCATCAGGGGAGGCTTTAGGGGG					
ss.AC003042	22990	23000	23010	23020	23030	23040
	TGATGAGATTTGAGCTGGGCCTCCAGAAAGTGGCTGTGGGGAGGGAGTGGGAGGGAAAG					
ss.AC003042	23050	23060	23070	23080	23090	23100
	CATGTCAGAAAATGGAATTTGATCCAATAAAAGCCTACAGATTGTCAGGTGTTGTGGGAG					
ss.AC003042	23110	23120	23130	23140	23150	23160
	TTTGGGGAACAGGGCATCATTTGGGTGGGTACAGCAAAGGGACTTCAAGAAGCCCAAAAG					
ss.AC003042	23170	23180	23190	23200	23210	23220
	GGGCCGGGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCAGGCAG					
ss.AC003042	23230	23240	23250	23260	23270	23280
	ATCATTTGAGGTCAGGAGTTCAAGACCAGCCTGACCCACATGGCGAAACCCCAACTCTAC					
ss.AC003042	23290	23300	23310	23320	23330	23340
	TAAAAATACAAAATTAGCCAGGCGTGGTTCGTGGGCACTTGTAATCCCAGCTACTCGGGA					
ss.AC003042	23350	23360	23370	23380	23390	23400
	GGCTGAGGCAGGAGAATCATTTGAACCCAGGAGGCGGAGTTTGCACTGAGCCGAGATCTT					
ss.AC003042	23410	23420	23430	23440	23450	23460
	GTCACTGCACTCTAGCCTGGACAGAGTAAGACTCTTTCTCAAAAAAAAAAAAAAAAAAAAA					
ss.AC003042	23470	23480	23490	23500	23510	23520
	AGAAGGAGGAGGAGAAGAAGAAGAAAAGGAGAAGGAGGAGGAGGAGGAGAAGAGGAAGAG					
ss.AC003042	23530	23540	23550	23560	23570	23580
	GAAGAAAGAAGATGAAGAGCGAAGAGGAAGAAGAAAAAGAAGAGGAAGAGGAAGAAGAAG					
ss.AC003042	23590	23600	23610	23620	23630	23640
	AGGAAGAGGAAGAAGAAGAAGGCGAAGGAGAAGGAGAAGGAGAAGAAAGAAGAACA					
ss.AC003042	23650	23660	23670	23680	23690	23700
	ACCAGACTGGGGCCAACTGTGGACAGTGTGACCATTATGCTCTGTACTTTATCGTGGAG					
ss.AC003042	23710	23720	23730	23740	23750	23760
	GCAATAGGGAGTTATTGAAGGTTTCTGAGCAGGGGTAGGCCATGATAGGATTTACATTTT					
	23770	23780	23790	23800	23810	23820

ss.AC003042	AGGCATATCAGGTAGAGAGAGAGCAGAGGTGAGGAGCCTACTGGAACCTCACTCCTCCAGC
ss.AC003042	23830 23840 23850 23860 23870 23880 ACATTGTTACTCTACTAACAAGAGCAGCACTTCTGACCTCGCTGGAGACTTTACAAAGCCT
ss.AC003042	23890 23900 23910 23920 23930 23940 TTTTCTTACCTTTACACACCAGACTTCAAGCTAGGTGGGTTCCTGACTCAAGCAGCTTT
ss.AC003042	23950 23960 23970 23980 23990 24000 GGGGTGAGGTGAAGCTCTGGGCTCTGGTTCCCACCCAGCTTCCTTCACGTCAGCATCCT
ss.AC003042	24010 24020 24030 24040 24050 24060 AGCATTGATTAAACAGTGTGCAAGTCCACCTGAAGGGTGGAGGGGTGGGGAGCTGGAAG
ss.AC003042	24070 24080 24090 24100 24110 24120 GAGCAGGAGTGGGGAGGGGAGGGTGCCCATGTACTCAGAGCCTGCTCAGTTCTTAGCCGT
ss.AC003042	24130 24140 24150 24160 24170 24180 TTCCTGCGCTCCTCACTGTGAAGGAATTATCCCTGTGCTACAAGAAGGAAAACGAGACCT
ss.AC003042	24190 24200 24210 24220 24230 24240 GGGAAAAGAAGAGCCCAGGACCCCCAGGGCCGGGACACAAGTCTGGGTGTGTCTGACCCC
ss.AC003042	24250 24260 24270 24280 24290 24300 AAAGCTCCTCATCCCAAAGCAAGAAGAGAAGCAGGCCTCAAAGAAGCCACACCCCTCAT
ss.AC003042	24310 24320 24330 24340 24350 24360 CTCTGAAGGAGACGCTGAAGGCCCTGTCTATCCAGCATCCCCTCCACCAGTCACAGCA
ss.AC003042	24370 24380 24390 24400 24410 24420 GACACCAGCCTCCTATGACATGCGTGCTCATGGATGCTCATGCTTTGAGAGACCCGGTTG
ss.AC003042	24430 24440 24450 24460 24470 24480 TACTGATGACATTCACAAAGAAGAAGTTTCATCTAACGTCCCATTTTGGATTTCATCAGCCT
ss.AC003042	24490 24500 24510 24520 24530 24540 CATCTGAGACTGTCAATCAGAGTCTCCATCCTGTGGCCAATGACACTGAGCAAGTGGCTG
ss.AC003042	24550 24560 24570 24580 24590 24600 GAGATGGCAAGGGGTGCTCAGGGTGGGGTCTATGCACAGAGCTGCCTTGGGGGACCCAG
ss.AC003042	24610 24620 24630 24640 24650 24660 GTGGGGCAGCTGACAGTCAGGAGGACTTCTGAGGAAGGGGTGGATGGCAGAAGGTAGAGT
ss.AC003042	24670 24680 24690 24700 24710 24720 TCTTGGAAGGTGATCACCTCTCCCCGTGCTGCTCATACCAGGTAGGCCCTGAAGG
ss.AC003042	24730 24740 24750 24760 24770 24780 GTGACAAGGGCAGCAGGTCTGAGGGAGGCTCCAGGACAGGGGAGAGACTGGACACAGAAT
ss.AC003042	24790 24800 24810 24820 24830 24840 CAGAGACAGGGTGAGAGACAGAGAAAGGGAGGTGGCGGTGCTTGTTTCACAGCTGGACTT
ss.AC003042	24850 24860 24870 24880 24890 24900 GGCGGTGGTGCCAGGGTGCTGGCCACACTCCAGCAGGGTAATAGCATCAGCTCCAGCCT
	24910 24920 24930 24940 24950 24960

ss.AC003042	AAACTTTAATCAATGAATCCAAGGCTTGGCCACAATCAGCAGTGAGGAAGATTAGCAGAA
ss.AC003042	24970 24980 24990 25000 25010 25020 TCCTGGGAGGGGAGAGGGACGGAAGTGCCCAGCCAAGGAAGACGGTGCATGGGATCTATT
ss.AC003042	25030 25040 25050 25060 25070 25080 GCAGGTCCGAGCGGGGGCTTCCAGTGCCCCCTTCCCACCGGGCATGAAGTGGAAGCAGAGG
ss.AC003042	25090 25100 25110 25120 25130 25140 TGGGAGTCAGACAGCTACATCAACAGCAAGGGAATGAATCTGGCCCACTGAGGCTCAGCG
ss.AC003042	25150 25160 25170 25180 25190 25200 AGACCCCAACACAGGCTCCAAGCCACTCTCCCCCAATCCCAACAAGCCTCAAGTGAGACA
ss.AC003042	25210 25220 25230 25240 25250 25260 CCAAGAAGAACTTACCAACCAGGGAGCCCCCAGGATGCCTGAGCAGGGGCAGCGCAAGGT
ss.AC003042	25270 25280 25290 25300 25310 25320 GTTACATCATCCCTACCTGGGCAGGGGTCCCAGCATAGGAGCTGGAGTGCCCCACCT
ss.AC003042	25330 25340 25350 25360 25370 25380 CCCCTTCAGGCTGGGCTGCACAGAGGGATGAACTGAATGGGTACATTCTTACCCCTCAA
ss.AC003042	25390 25400 25410 25420 25430 25440 GTGCTTTGGAGAGAGGGTAGAAGGAAGGAGGAGACAAACCAGTTATCATCTGCCCTACAT
ss.AC003042	25450 25460 25470 25480 25490 25500 AACTTATTAGCATCCAGGCGAGATTAATCAAGCCCAGAAACCTCGAGCACACCCCTAATT
ss.AC003042	25510 25520 25530 25540 25550 25560 AGTTGCTGCTGATAACTATATTTGTCATGCTTTCCAATTATTCCACTGTAAATTTTCAGAG
ss.AC003042	25570 25580 25590 25600 25610 25620 TTTAATTGCACCTTGTTCTTCATTGAAGTGTCACTGTTTGCACACGCTCCCCTAATTCTT
ss.AC003042	25630 25640 25650 25660 25670 25680 TAGCAAATTTGACAAAATTACAGATTAAATATAGATTATCTTTAGATTTCCATAATTAAC
ss.AC003042	25690 25700 25710 25720 25730 25740 ACAACCAAACGTCTCAGGCCTAAATATTTCTCCCAGTATCATAAATCTGGCCTGTCCCT
ss.AC003042	25750 25760 25770 25780 25790 25800 GGAATCCGAAGGGCTGCTTCCAGCTCCCCGGCAGAGGCTGCAGGGAGAACACACATGCAC
ss.AC003042	25810 25820 25830 25840 25850 25860 AGCCATGAACTCACATGACACGCCTGTGCAGGGCTGGGGCAAAGGCGGCAGTGATACTT
ss.AC003042	25870 25880 25890 25900 25910 25920 CATTGAGGGCACACAACCTGGGAACATACCCCGTGCCCCATATCAGTAGGGGCTCCATCAA
ss.AC003042	25930 25940 25950 25960 25970 25980 GATGCCCCACCTGGGGCGTGGGGCAGTGTCCCAGGGCTTGAGGGCCAATTCAGGATCGC
ss.AC003042	25990 26000 26010 26020 26030 26040 AGCTGACCTCTGCGCCTAGCGAATGGGCTAGAGGGAAGAGGCTCGGCCTACAACCAGATC
	26050 26060 26070 26080 26090 26100

ss.AC003042	ACAAGCCTCCCCACCCAACAAAGGCCAAAGGGCCCCCTTCTGTGACTTTTTTTTGTCCCTG
ss.AC003042	<div>26110 26120 26130 26140 26150 26160</div> TCAAGGCTGACCTTGATGTTTGACATTACCCCAGGAGCATGACCCAGGCAGACATGAATG
ss.AC003042	<div>26170 26180 26190 26200 26210 26220</div> CCCTCATGCCATAACCCCTGCAGGGCACCGCCACTGCCCAGCCTTCTCTCTTAGTCCGCTC
ss.AC003042	<div>26230 26240 26250 26260 26270 26280</div> TCTCCAGACTCACCAGGCAAGTATATGTCCATCCAACCTCTAACTGTCCCCACCTGGGAC
ss.AC003042	<div>26290 26300 26310 26320 26330 26340</div> CCTTTAGTTCAGATTAGGGGATGAAGGAATCCGACATCAGGTTTGAAATGATGCCCCCAT
ss.AC003042	<div>26350 26360 26370 26380 26390 26400</div> ATGAGGTTTGAATTTTTTTTTTTTTTTTTTTGAGACGGAGTCTTGCTCTGTTGCCCAGGCT
ss.AC003042	<div>26410 26420 26430 26440 26450 26460</div> AGAGTCCAGTGGCTTGATCTCAGCTCACTGCAACCTCTGCCTCCTGGGTTCAGTGATTA
ss.AC003042	<div>26470 26480 26490 26500 26510 26520</div> TCCTGTCTCAGCCTCCTGAGTAGCTGGGATTACAGGTGCGCACCACCATGCCCAGCTAAT
ss.AC003042	<div>26530 26540 26550 26560 26570 26580</div> TTTTGTATTTTGTAGTAGAGATGGGGTTTCACCATGTTGCCCAGGCTGGTCTTGAATTCT
ss.AC003042	<div>26590 26600 26610 26620 26630 26640</div> GACCTCAGGTGATCCACACACCTCGGCCTCCCAAAGTACTGGGATTACAGGTGTGAGCCA
ss.AC003042	<div>26650 26660 26670 26680 26690 26700</div> CCACGCCAGTCTGAAGTCTCTTCCACCAGCCCCCAAACCCCAAATCTAACATCGCAAG
ss.AC003042	<div>26710 26720 26730 26740 26750 26760</div> GAAATCAGCAGGGTGTCCTTTCCATAGGGACAGGAGGGGGCAGGAGGCAGCAGGGAAG
ss.AC003042	<div>26770 26780 26790 26800 26810 26820</div> CCTGTGCCCTTTTCAGATCCCAGCCCAGCCTCTGGCCCTGGTGGAGGAGAATCATATCT
ss.AC003042	<div>26830 26840 26850 26860 26870 26880</div> TGGGTTTATCCCAAGTCAAGCCCCTTCCCCAGGCTGGCTATCTCATGGGCAGCAGAGCAT
ss.AC003042	<div>26890 26900 26910 26920 26930 26940</div> CCAGAGTTCAACTGCAAGCCCAGCCCCCATGCCCCCTGCAGTCACGCAAACACACCTGT
ss.AC003042	<div>26950 26960 26970 26980 26990 27000</div> ACACACAGAGGCAGATGCACAGATGCAGAAATGGAAAGACACAGATGCACAGAGACACAC
ss.AC003042	<div>27010 27020 27030 27040 27050 27060</div> CACAGAGATACACACAAAACACAAACTGACACACAGACAGATACACAATGCAACACACAG
ss.AC003042	<div>27070 27080 27090 27100 27110 27120</div> CCCAAGCCCTGTAGGAAGACGGGGATAGACAGACGGGGAAATACTCCCTCCCCAGAAATC
ss.AC003042	<div>27130 27140 27150 27160 27170 27180</div> AGTGACATACCCAGGGTCTTGCCACATTGAAGGGCCAAGGGGGGCTGGGGGCCCCCTTGC
	<div>27190 27200 27210 27220 27230 27240</div>

ss.AC003042	CCTCCATGCCACCTGCCAACCCCTGACACCCCTGTTTCCCCGGCGTAGCTGCAGGGGTAGT
ss.AC003042	<div>27250 27260 27270 27280 27290 27300</div> TGAGGGGCTGAGGTGGGAGCAGGCAGGAATACAGAAGAGCCTCAAAGTGTACTCACAGCA
ss.AC003042	<div>27310 27320 27330 27340 27350 27360</div> AATTTGGAAGAAAATCGATGGCCTTTAATGAGATTTGATTTTTTCTCCACAATGGGCTGG
ss.AC003042	<div>27370 27380 27390 27400 27410 27420</div> GCTGGTGGTTGTGGGGGATCTCTGGGTGCAATGTGCAAGGAAGTGAGCAGGGGCACAAG
ss.AC003042	<div>27430 27440 27450 27460 27470 27480</div> GTGCAGGGCTGAGAGGGACTGGGAAGCCGGGAGTGGGGAAACACCAGGGTCAGCAGCTAC
ss.AC003042	<div>27490 27500 27510 27520 27530 27540</div> AGGGACAGGAAGAGGCAGAGGATAGACAGACAGGCAGGATGTCAGTGTGAGGCCGTCACT
ss.AC003042	<div>27550 27560 27570 27580 27590 27600</div> TAGCCCCACCTGTCAGAACAAGAGAGGGGCCCTGAGCTGGCTTGGGTGTATACTGTGGCC
ss.AC003042	<div>27610 27620 27630 27640 27650 27660</div> CTGTTGGGTTCTAGATGCGGAGTCTGCACTCCCAGCCCTCAGTAGGAGATAAAAGGCTGA
ss.AC003042	<div>27670 27680 27690 27700 27710 27720</div> GGTTCATCCAGGTTATGAGGCTGGCAGGGACCAAGCCATGGGGAGCAGTCACAGGATGGG
ss.AC003042	<div>27730 27740 27750 27760 27770 27780</div> GTATGTTGGGGGTGTGGCTGGCTTGGGTCCTTGGCTTCCAAGGTTGCTAAAAGGAAAATT
ss.AC003042	<div>27790 27800 27810 27820 27830 27840</div> GTAAGGAGCTTAATTCTGATCAGTGCAGTTAACTGAGCACCTGCCAGGCTCCAGGCCCT
ss.AC003042	<div>27850 27860 27870 27880 27890 27900</div> GTTATTGTTATTCTGCAGGAAACCCACAAGAGAGGTGACAACCCCTTGCTCCCAGATGA
ss.AC003042	<div>27910 27920 27930 27940 27950 27960</div> AGAAAATTAGGATCAGAGACATTAAAGAAAATTGCCCAAAGCCACTCAGCCAATGGCTGAG
ss.AC003042	<div>27970 27980 27990 28000 28010 28020</div> GCAGCAACTGAACCAAGGTCCACCAGATTCTAAAGTCTGTTTCTTCCGTTCTGCCTGCAA
ss.AC003042	<div>28030 28040 28050 28060 28070 28080</div> GCAGCACCTGGCAGGCGATGGAGGCACATCTTAGTCTCTCTTCTCTCTCCAGTCCAGG
ss.AC003042	<div>28090 28100 28110 28120 28130 28140</div> TCTCCAAGACCTATGGATGGGTTGGGCCAGGGCTTGGGTTGAGGCTCCAGGGTGATGGCA
ss.AC003042	<div>28150 28160 28170 28180 28190 28200</div> ACTTAAGGGAATCTCCTGCACAGCTAGGCTTCAAAGCACAAAGACTTCCCCAGGCACAGAG
ss.AC003042	<div>28210 28220 28230 28240 28250 28260</div> GAGGGCATACTATCAGCTGCAGCCCCGTCCATCCCACCCTGCTGGCTGAACCTTTGAGC
ss.AC003042	<div>28270 28280 28290 28300 28310 28320</div> TCCCTCCTTCCTTATGGAATCATAGAAGGGATCAGAGGCCATCAACCCCAAACATATCTT
	<div>28330 28340 28350 28360 28370 28380</div>

ss.AC003042	CTGTCTGAAGCCCCTGTGAAATATTCTGAGTGATCAACTGAGGTCTCGCACAACCTCTAGT
ss.AC003042	28390 28400 28410 28420 28430 28440 GACAGGGAGCTCACTACCTCCAAGGTATCCTCTTCCACTTCTGGAATCTTGCTAGATTGA
ss.AC003042	28450 28460 28470 28480 28490 28500 GCTGCTTTTTTGCTCCCTGGGCCTCCTACTGGTCCTGTTTCTGCCTTCTGGGTCATCACT
ss.AC003042	28510 28520 28530 28540 28550 28560 CTGCTCCACGAAAGCCCCTCTGTAAGTGAATACCACAATCACTGCCTTCCCACCACCTG
ss.AC003042	28570 28580 28590 28600 28610 28620 GGGGCTTCCATGCTCCTGGCTAAACACGTCATCATTCCTCAACTGTTGCAATAGTCCCT
ss.AC003042	28630 28640 28650 28660 28670 28680 GACCATTCCCTCCCACCCACCCAAAGGCAGAATTATTGACAGCATAAAGGAGTGGTTTGG
ss.AC003042	28690 28700 28710 28720 28730 28740 CAATGATTTCTTATGACATCAAAAGCACAGGTAACAAAAGCAGAAGTAGAAAAATAGGAT
ss.AC003042	28750 28760 28770 28780 28790 28800 TACATCAAAATGTAACTGTGCATCCAGGAATACAACCCGCAGAGTGAAAAGGCCACCTA
ss.AC003042	28810 28820 28830 28840 28850 28860 CACAATGGGAGAGAATACTAGCAAATCTTATAACTGATAAGAGGTTAATATTCAGAATAT
ss.AC003042	28870 28880 28890 28900 28910 28920 ATAAGGAACTCCTACAACCTCAATAGCAAAAAAGTAAACAACCTGATGTAAAAATGAACAA
ss.AC003042	28930 28940 28950 28960 28970 28980 AGAGCACGAATGGACATTTCTCCAAAGACGACACACAAGTGGCCAGCAAGCCTATGAAAA
ss.AC003042	28990 29000 29010 29020 29030 29040 GATGCCCCGACATCACAAATGACCGGAAAAACGTAAATCAAACCAAGGAGATGCCGCC
ss.AC003042	29050 29060 29070 29080 29090 29100 TCGCATCCATTATGATGGCCACCATCAGAAAAGACAGAAAAATAAACAGTCTTATTGAGGAT
ss.AC003042	29110 29120 29130 29140 29150 29160 GTGGAGAACTGGAACCTTGAGCACTCTTGGGGGCAGTGTAATAATGGTGCAGCTTCTAT
ss.AC003042	29170 29180 29190 29200 29210 29220 GGAAAACAGTATGCAATTCCCTCACAAAATTAAAAATAGAATTATAATCGGATCAGCAATC
ss.AC003042	29230 29240 29250 29260 29270 29280 CCACTTCTGGGTATATATTGAAAGAACTGAAGGCAGCGTCTTTTTTTTTTTTTCTTTTT
ss.AC003042	29290 29300 29310 29320 29330 29340 GAGACTCACTCTGTGCCCCAGGCTAGAGTGCAGTGGTGCATCTTGGCTCACTGCAACCT
ss.AC003042	29350 29360 29370 29380 29390 29400 CCGCCTCCTAGGTTCAAGCAATTCTCCTGCCTCAGCTTTCCAAGTAGCTGGGATTACAGG
ss.AC003042	29410 29420 29430 29440 29450 29460 CATGCGCTACCACACCTGGCTAATTTTTGTATTTTTAGTAGAGATGGGGTTTTGCCATGT
	29470 29480 29490 29500 29510 29520

ss.AC003042	TGGCCAGGCTGGTCTTGAACCCCTGACCTCAAGTTATCCATCCACCTTGGCCTTCCAAAG
ss.AC003042	<div>29530 29540 29550 29560 29570 29580</div> TGCTAGGATTACAGGCATGAGCCACTGCACCTGGCCCAAGGCAGGGTCTTGAAGCGATAT
ss.AC003042	<div>29590 29600 29610 29620 29630 29640</div> TTGCACACCCATGTTTCTAGCAGCATTATTCAAAAAGCCAAGAGGCAGAAGCAACCCAG
ss.AC003042	<div>29650 29660 29670 29680 29690 29700</div> GTGCCCATCGATGGATGGATGGATAAACAAATGTGGTGTACACAGACAATGAAATATTA
ss.AC003042	<div>29710 29720 29730 29740 29750 29760</div> TTCAGTCTTAAAAAGGAAGGAAATTCTGTCACATGCCACAATATGGACAAACCTTGAAGA
ss.AC003042	<div>29770 29780 29790 29800 29810 29820</div> CATGATGCTAAAATAAGCCAGTCACAAAAGACAAATGCTGTATGATTCCACTCTATGGG
ss.AC003042	<div>29830 29840 29850 29860 29870 29880</div> GTATCTAAAGTCATCCAATTCATAGAAACAGAACAGAGAATGGTGTGGTGGCAAGGGCTGG
ss.AC003042	<div>29890 29900 29910 29920 29930 29940</div> GTGGTGGATGGGGAGCTGCGGTTTAAAGGGTAGAGTTTCCGTTTTGTAAGGCAAAAGAGC
ss.AC003042	<div>29950 29960 29970 29980 29990 30000</div> TCTGCAGAGCTGTTGCACAGCAATGTGAATATACTTAACACTACTGACTGGTACACTTAA
ss.AC003042	<div>30010 30020 30030 30040 30050 30060</div> AAACAGCTAAGACAATAACAACAAAGCCACAATTCTGGAGTCAGACTTGGGTTTGAGTT
ss.AC003042	<div>30070 30080 30090 30100 30110 30120</div> CCAGCTCTGTCACATGGCCTGGGGCAAGTTGTCAAATGTCTCTAAGCCTCAGTCTCCCCA
ss.AC003042	<div>30130 30140 30150 30160 30170 30180</div> GCTTTACAACAGGGTAATGATAGAACCTAATTCACACGATCTCATCGACAAAGCAGGTGA
ss.AC003042	<div>30190 30200 30210 30220 30230 30240</div> AGTGTCTGGGACCTGGTCAGTTGGCTCTGGAACCATGTTCTGGAAGCTACCCTTGACGG
ss.AC003042	<div>30250 30260 30270 30280 30290 30300</div> AGGCTGCGCAGGTTGGAGTTGGGCAGCTTCCAGCCCTGGGCTGTCCGCTCCCAGTGGCAC
ss.AC003042	<div>30310 30320 30330 30340 30350 30360</div> CCAGCCTCTATTTCCGTGACCTCTCCGTCTGTCCATTTCTCTCACTGTCTCCCTCCT
ss.AC003042	<div>30370 30380 30390 30400 30410 30420</div> TACCTCTCTCCAGCCACGCTGGCCTAGAGCACACCAGGCACACTCCTACCCAGAAGCCTT
ss.AC003042	<div>30430 30440 30450 30460 30470 30480</div> TGCACTTAGAGTTTCCACTGCTTCAAATGCTCTCAGGGACTCACTTCTGCCCTTTCTCCA
ss.AC003042	<div>30490 30500 30510 30520 30530 30540</div> GGTCTTTGTTTACAGTCCCCCTGTTTAAATTTGTGCCCTCCCCCAACCACGGGGCTCTAT
ss.AC003042	<div>30550 30560 30570 30580 30590 30600</div> GTCCCCTTCCCCTGCTCTACTTTTCTTACAACATACTATATAATTTTACTTATTGGTTGT
	<div>30610 30620 30630 30640 30650 30660</div>

ss.AC003042	CGCTGACTTGCTCACTGCTATATCCCCAGCTGGCACAGAGTAGGTGCTCAATAAATACTT
	30670 30680 30690 30700 30710 30720
ss.AC003042	GATGAATGACAGCCTAAGCTAAGCCTTGGCATTCTGTCCTTAGAGGCCCTCTGCCCCAG
	30730 30740 30750 30760 30770 30780
ss.AC003042	CCCCAAATTTTCATCATTGTGGTGTCTGCCCCCTTAAGGACTCCCACTCCCAGGTCCCCCTT
	30790 30800 30810 30820 30830 30840
ss.AC003042	AAGGACTCACACTCCCAGGTCCCCTCAAGGACTCCCACTCCCAGGTCCCCTCAAGTGTGG
	30850 30860 30870 30880 30890 30900
ss.AC003042	GGGGAGAACCCCACTTCCCCCTAAAGCCCCAGGCTGCCCAGCTGCTGCTCCACTGGGACC
	30910 30920 30930 30940 30950 30960
ss.AC003042	TCAGCACCAATTCTGCCCATCAATATCAGCCTGCAGCAGTCACACTTGAACACCCACCCC
	30970 30980 30990 31000 31010 31020
ss.AC003042	AATCGATAACCAGCGGCTGCTATCGATCAGCCCCGAGGGCACAGGAAGCCGGTGGGGAGA
	31030 31040 31050 31060 31070 31080
ss.AC003042	GGGAAGGAGAGGACCAGGCATGGTGTGCGGACACAGCCTCAGAGAGGGAGCAACAGCAAA
	31090 31100 31110 31120 31130 31140
ss.AC003042	GAGCCCCCAGTGACCCGGCCAGGGCAGGCAGACAGGACAGAGCTCATCAGAAACCAGAGG
	31150 31160 31170 31180 31190 31200
ss.AC003042	CAGAGGTGAAGGGGGAGGAGAAGCCAGACCCCAGGCTAGGAAGGGCAAAGGGGCAGACAC
	31210 31220 31230 31240 31250 31260
ss.AC003042	AGAGGGAGGCTGCTGAGAAGAAGGAAGAGGCAAGATAGGAAGGGTTGGCCAGGCGCAGTG
	31270 31280 31290 31300 31310 31320
ss.AC003042	GCTCATGACTGTAATCCCAGCACTTTGGGAAGCCAAAGCGGGTGGATCACTTGAGGTCAG
	31330 31340 31350 31360 31370 31380
ss.AC003042	GAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCCCGCCTCTACTCAAATACAAAAAT
	31390 31400 31410 31420 31430 31440
ss.AC003042	TAGACAGGTGTGGTTGTGGTGGGAGCCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGG
	31450 31460 31470 31480 31490 31500
ss.AC003042	AGAATCACTTGAACCTGGGAGGCGGAGGTTGCAGTGAGCAGAGATCAGGACACCGCACTC
	31510 31520 31530 31540 31550 31560
ss.AC003042	CAGCCTGGGTAACAGAGCGAGATTCCGTCTCAAAAAAAAAAAAAAAAAAGACGGAAAGGAA
	31570 31580 31590 31600 31610 31620
ss.AC003042	GGAAGGGTTATTGAAGGTCTACCATATGCCAAGGGCATCATCTCTCAAGCCTCCCAGCAC
	31630 31640 31650 31660 31670 31680
ss.AC003042	AACCGTGGGTGAAAGCAGTTATTGGCTCTATCTTACAGGGAGGAACTAAGCTCAGAGGT
	31690 31700 31710 31720 31730 31740
ss.AC003042	TAAGAACTCACCCCAGGCCTGAGCCTTCAAATCTGGGAGCAGAGCCAGGATTTGAACCC
	31750 31760 31770 31780 31790 31800

ss.AC003042	ATGTCTGGAGTCTCTGTGGGGCCAAGGCTCTTTGCAGCACCCACAGTAGCTCTGAGCTG
ss.AC003042	<div>31810 31820 31830 31840 31850 31860</div> TCACTTCTGGGCTTCCAGCCTGGAACACCACCTAAAGCCAGTGGGAACTGGATGGAGGT
ss.AC003042	<div>31870 31880 31890 31900 31910 31920</div> GCCTCCCAGCACCTCCACTGGAATGTCCCACTTAGAGCTTGTCAAGGTAGCTCGGAAAGC
ss.AC003042	<div>31930 31940 31950 31960 31970 31980</div> CTGGGCGGTGGTTTCATGCCTGTAATCCCAGCTACTCGGGAGGCCGAGGCAGGAGGATCAC
ss.AC003042	<div>31990 32000 32010 32020 32030 32040</div> TTGAGCTCAGGAGTTCAAGGCCAGCCTGGGCAACATAGGGAGATCCCATCTCAACAACAA
ss.AC003042	<div>32050 32060 32070 32080 32090 32100</div> CAAAACGTTTTTAATCAGCTGGGCATAGTGGCTAAGGAGGCTACTCAGGAGGCTGAGGT
ss.AC003042	<div>32110 32120 32130 32140 32150 32160</div> GGGAGGATCACTTGAGCCCGGAGTTGGAGGCTGCAGTGAGCTATGATTGCATCACTGCAC
ss.AC003042	<div>32170 32180 32190 32200 32210 32220</div> TCCAGCCTGGGCAACAGAGCAAGACCCTGTCTATAAAAGAAAACAAACAAACAAACAAA
ss.AC003042	<div>32230 32240 32250 32260 32270 32280</div> AGTATGGTAAGGGAAACAAGATGAGGCATGTAAGCCCATGGTAAGTGCATAACAAATGCT
ss.AC003042	<div>32290 32300 32310 32320 32330 32340</div> AGTACCATCATCATCACCATCACTCCTCCTCCTGTTCCAAGCACACGGCTTCCAGGTC
ss.AC003042	<div>32350 32360 32370 32380 32390 32400</div> GCACACTCACTGAAGCGAGACTGTTGTTAAGAGTGTGTGTCGGCCTCAGGGCTCTGATTC
ss.AC003042	<div>32410 32420 32430 32440 32450 32460</div> AGACAAGATCCAGCCCCATGCACAGTGCCTGACCCAGGCTAATACCTGTATCTATGCAAG
ss.AC003042	<div>32470 32480 32490 32500 32510 32520</div> GGGCTGTGCGACGGAAAGTCTGGCACAGGTGGGTCTCTGCAGAGCTGAGGGGCTGAGGGAG
ss.AC003042	<div>32530 32540 32550 32560 32570 32580</div> GCTGTGAAGCATCTCCTCAGCCTCAATTAGCTCCCTTGTTTCAGAGAAGCAAGACCAGCT
ss.AC003042	<div>32590 32600 32610 32620 32630 32640</div> GTGGCTGGGGATGATTTCTGACTTGCCCTCCTCTGACACTGCTTGAAAGTGGGAAGGTCAAG
ss.AC003042	<div>32650 32660 32670 32680 32690 32700</div> GCCGGCTGGAGGCGTGCTCAGGGATCTGCCCTCCAGCCCACTTCAGAGAAGAGGAAGAG
ss.AC003042	<div>32710 32720 32730 32740 32750 32760</div> GAGGCAATCAGCCTCCAACCTCAGGACTTATCACTTGTTTCATGCATCATTTGTGAAACAC
ss.AC003042	<div>32770 32780 32790 32800 32810 32820</div> CCAGCACGTGCCTGGCCCTGTGGTGGGACCTGGGAATACAAAATCAGTAAGGGTGATTCC
ss.AC003042	<div>32830 32840 32850 32860 32870 32880</div> TGCTTGAAGGTCTAAGTGGGGCAGGGATATTCTAGAGGGCGGGAGGGGCTTATGTGTCT
	<div>32890 32900 32910 32920 32930 32940</div>

ss.AC003042	GCGGTTGTAGGGAGCAGGCGGCCTGCAAGAAAGTTTTGTTGTCGTTGTTGTTGTTGTTGT
ss.AC003042	<div>32950 32960 32970 32980 32990 33000</div> TGTGTTGTTGTTGAGACAGTCTCACTCTGTGCGCCAGGCTGGAGTGCAGTGGCGTGATCTC
ss.AC003042	<div>33010 33020 33030 33040 33050 33060</div> AGCTCACTGCAACCTCTGCCTCCCAGGTTCAAGTGATTCTCCTGCCTCAGCCTCCCAGT
ss.AC003042	<div>33070 33080 33090 33100 33110 33120</div> AGCTGGGATTACAGGAATGCACCATGCCCAGCTAATTTTTGTATTTTTAGTAGAGATGAA
ss.AC003042	<div>33130 33140 33150 33160 33170 33180</div> GTTTCACTATGTTGACCAGGCTGGTCTTGAACCTCTGACCTCAGGTGATCCACCTGCCTC
ss.AC003042	<div>33190 33200 33210 33220 33230 33240</div> GGCCTCCCAAAGTACTGGGATTACAGGCATGAGCCACCACGCCTGGCTTAGTTTCCTCTT
ss.AC003042	<div>33250 33260 33270 33280 33290 33300</div> TCTAAGGGGAGCTGTTTAGCCCATGAATTTTTTTTTTTTTTTGAGACGGAGTTTTGCTCT
ss.AC003042	<div>33310 33320 33330 33340 33350 33360</div> TGTTGCCCAGGCTGGAGTGCAATAGCGCGATCTCAGCTCACCGTAACCTCCGCCTACTGG
ss.AC003042	<div>33370 33380 33390 33400 33410 33420</div> GTTCCAGGGATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTATAGGCGCCTGCCATC
ss.AC003042	<div>33430 33440 33450 33460 33470 33480</div> ATGCCCAGCTAATTTTTGTATTTATAGTAGAGATGGGGTTTCTCCATGTTGGTCAGGCTG
ss.AC003042	<div>33490 33500 33510 33520 33530 33540</div> GTCTCAAACCTCTGACCTCATGATTGCGCCACCTCGGCCTCCCAAAGCGCTGAGATTACA
ss.AC003042	<div>33550 33560 33570 33580 33590 33600</div> GGCATGAGCCACCGCGCCCGCCAGCCCATGGATTTTTTTCTCAGGTTGCAGATAAACCAC
ss.AC003042	<div>33610 33620 33630 33640 33650 33660</div> AAAGGTACTGCTTCTCATGGAATCTCCCTTCTGATGCCTACAAACCTTACCAAGAAAGCT
ss.AC003042	<div>33670 33680 33690 33700 33710 33720</div> GGAGCCCGAAGGGGGAGAAGGGCCAGACTGCAGAGAGGGCAGGAGAAAGACAGGCCCAGC
ss.AC003042	<div>33730 33740 33750 33760 33770 33780</div> CCCTCCTCCCCGGCCACAGCAGCTGGTGAAGGGTGTCCTCTGAAATGGAATACTGTGAC
ss.AC003042	<div>33790 33800 33810 33820 33830 33840</div> CGAGAGGGCACATGGCAGGGGCGAAGGACAGGCATTTCCATAAAAAATCCTTGGAGTGCAG
ss.AC003042	<div>33850 33860 33870 33880 33890 33900</div> TCAGGAGGAGTCTGTTTCAAAGCAGCCTTTGCAGAGCCTGAGGTAGAAATCTCTGGTC
ss.AC003042	<div>33910 33920 33930 33940 33950 33960</div> CTGATTCAAAGAGCAGCCCCCTCTCCCTTTCCCAATCTGGGGAAGGAGCTGAGCCAATTAA
ss.AC003042	<div>33970 33980 33990 34000 34010 34020</div> CTGGGAGGCAGAGCTCGAGCCCTTTCCAGCTTCTCTGGAGGTGCTAATGGTCCTCAGGGC
	<div>34030 34040 34050 34060 34070 34080</div>

ss.AC003042	TCTGGCCCTGCTCCCCCTCCACCCACCCCCAATGGGCTACATACAGTTCTGCGATTTAAG
ss.AC003042	34090 34100 34110 34120 34130 34140 AACATAGTTTTGAGAGCAGTTGTTTTGCCCATAAAATAACTACAATATTTGAGCAAATAA
ss.AC003042	34150 34160 34170 34180 34190 34200 ATATTTTATTTGCCCATAAAATAACTACAATTATTGAGAGTTTACAATTTACTGGGCACT
ss.AC003042	34210 34220 34230 34240 34250 34260 GTGCTAACCCCTGTGAGGTATGACATCCTCATTTTACAGAAGAGACAATAAATGTCCT
ss.AC003042	34270 34280 34290 34300 34310 34320 AGAGGACAAGCATCTTGCCCTGGGCATCCAGCTAGCAAGAGATGGGTGGGATGGGAACCT
ss.AC003042	34330 34340 34350 34360 34370 34380 GAGACTGCGCCCTGTTACAGGGGGATTCTGAAGGAAGGGAAAGTGGCCATGTTGGGGTG
ss.AC003042	34390 34400 34410 34420 34430 34440 CCCAGGAGATGGGGGATTAAACCTATGGATTAGAGGTTGAGGGAAGAGGATAAAAGGAA
ss.AC003042	34450 34460 34470 34480 34490 34500 GGATCCGCTCCAGGTGCTTCGTCCCCTGACCAGGTTTCCAGGACCCTCAGGAGAGGGGGA
ss.AC003042	34510 34520 34530 34540 34550 34560 CAGTGACAACCTCTGGTCAGCGGCAACATAAACTGCCTCTATGTCACCTGGCGCACAG
ss.AC003042	34570 34580 34590 34600 34610 34620 GCCCAGAAGTGAGAGGCACTGAGCTCTGGGCTGGGTAGGAGGCCGTTAGAATTTCTGGA
ss.AC003042	34630 34640 34650 34660 34670 34680 GCACCTCCCCCAGCAGGATGAGCTGAAGACCCTAGGGAGGTGTTAATGAAACAGGGGAAG
ss.AC003042	34690 34700 34710 34720 34730 34740 CTGCAAACAGACCCAGGAGTGATTCCAATCTGACACCTCCCCCTACGCAGCCCCACCAG
ss.AC003042	34750 34760 34770 34780 34790 34800 TAATGAGCTGGGACTTGCCCTTCCCCCAGAGAGCAGGGTGAGGGGAGGAGGAGCGTTC
ss.AC003042	34810 34820 34830 34840 34850 34860 TTGGGCATTTTTTTTTTAGCTTCAAAGCCTCTTTTCATCATCATCGTCATCATTGTCATC
ss.AC003042	34870 34880 34890 34900 34910 34920 GTCATCATCGCATTGAAAAGCTCACATTTATTGAACACCTACTGTGTCCCGGGCACTGTG
ss.AC003042	34930 34940 34950 34960 34970 34980 CTAAGTCTTTTTCATGTATCCCATCATTAATCCTCACATACAAACCTTAAGCCTACATGG
ss.AC003042	34990 35000 35010 35020 35030 35040 TAGGTAGTATTCTTATCTCCATTTTGCAGATTAAGAACTGAGGCTCAATCAGGGTAAGT
ss.AC003042	35050 35060 35070 35080 35090 35100 GACTTGCCCTAAGGTAGGGCCCACATGTGGAGCCGGCACTGTCTGACATCCTGCTTTTGGT
ss.AC003042	35110 35120 35130 35140 35150 35160 ACCGGACTTCTGACCCACCGAGAACTCCTGCAGGGGGACATGTTTGTGTGGCCTCAGGGC
	35170 35180 35190 35200 35210 35220

ss.AC003042	TGCAGCTGAGTGGTGAATAAAGGCAGCGCGCCAGTACACATCCTTGAAGTTCAGAATTG
ss.AC003042	<div>35230 35240 35250 35260 35270 35280</div> GGAAGAAAGACACTGGTAGACTGAGTCGGTGGGACAGGGATGAGTAGGATCCTGGCCTTG
ss.AC003042	<div>35290 35300 35310 35320 35330 35340</div> CCGCCAAGCCTCCCTGTCTGCTTTCCCTGCTCTCCGCTTCCACATGTGTACTGAGAAG
ss.AC003042	<div>35350 35360 35370 35380 35390 35400</div> GGGCCAGGAAGCTCGGGGAAGGAGGAGGAGGGACCTCTAGCTCTGTTCACTGCCTGGGGA
ss.AC003042	<div>35410 35420 35430 35440 35450 35460</div> AGGGGAGGCAGAGGGGTTCTGGCTGGGGAGGAGGCCTGAAGAAGTGGGGAGAGGTTGCAG
ss.AC003042	<div>35470 35480 35490 35500 35510 35520</div> GGAAGACCCCTGCCTCACAACCCCAGGAGGGAGTGGCTGAGCGGCTCTGCAGTGGAGCCC
ss.AC003042	<div>35530 35540 35550 35560 35570 35580</div> CATGTTTGTAACACCATTAATCAGGGATTAGCAGATGGGCATGCTAATTGCACCTGTGG
ss.AC003042	<div>35590 35600 35610 35620 35630 35640</div> AAGTGAGAAACCTCAAGGTTGATTACATTTACAAACTGTGGGGATCCCTGGCACCTGGCC
ss.AC003042	<div>35650 35660 35670 35680 35690 35700</div> CTGCAGGAGTCGGTGGTGGTAGTGGTGGTGTGTGTGTATGTGTGTCGGCGAAGCGGGGGT
ss.AC003042	<div>35710 35720 35730 35740 35750 35760</div> GGCGGGTGTGCTGTCTAATTCAGGACCCCAACCTAGGGGGAGGGGGATTGACAATTTAGC
ss.AC003042	<div>35770 35780 35790 35800 35810 35820</div> CTCCTGCCAAAAAATATTCCAGGCCTGCAGCAGGGATCTGGGGTGCCAGCCTTGATTTA
ss.AC003042	<div>35830 35840 35850 35860 35870 35880</div> GCTGCTCCGAGAATACCAAGTCACTGCCAATTCTTCTTAGACCCTTTCCATCTCGGCATC
ss.AC003042	<div>35890 35900 35910 35920 35930 35940</div> TCAGGATCTTGAGCCCCTGACAAAGGGGGATCCTACAAATGTCATTCCAACCCCTCTCCT
ss.AC003042	<div>35950 35960 35970 35980 35990 36000</div> CCCTCAACTCCCTCCAGCAGTTCCCAGTGGTAAATCATTGTGCACTACAGATGAAAGGGG
ss.AC003042	<div>36010 36020 36030 36040 36050 36060</div> CCAGAGCCTACAGGAAAACGGAGGCCAGGTTGGTTGGGAAGCACAAACCAGCACCCCTGAC
ss.AC003042	<div>36070 36080 36090 36100 36110 36120</div> CTCTAAATCTGGCCCTAGAGGCTTTGAGGAGCAGCTACCATGCTCCTCCAGGCATGGGGC
ss.AC003042	<div>36130 36140 36150 36160 36170 36180</div> TGAGGGTTTTACATGTATGACCTCTTTCAATCCATACCACCATCCTTTGAAGTGGACACC
ss.AC003042	<div>36190 36200 36210 36220 36230 36240</div> ACTGTCATCCCCATTTTATAGGCGATGAAAACCTGAGGCTTGGAATTTAAGGGACATGTCC
ss.AC003042	<div>36250 36260 36270 36280 36290 36300</div> ACATTTATACTTCTAGCAAGCCACAGAGTTGGAACCTCAAAGCAAGCACTGTCTAGCAGCC
	<div>36310 36320 36330 36340 36350 36360</div>

ss.AC003042	AGGCTCCTGCTCTTAACCACCACTGCTCTCTCCTCTGACTTCATTCCAACCTCTGCCCTGC
ss.AC003042	<div>36370 36380 36390 36400 36410 36420</div> AGGGGATGGACCCCCACCCAGCCCCTTCACACCCACAGCCACAGCCTCCCCAGCTCCCGT
ss.AC003042	<div>36430 36440 36450 36460 36470 36480</div> GTACTTAACCCACACTTGCTGAGCAGTGTCCACTCAGTGTATAGGCACCGCGCCAGGTAC
ss.AC003042	<div>36490 36500 36510 36520 36530 36540</div> CAGAGGCTGCCTAAAGGAGAATCAGGCCTCATCCTCCTCATCCTTAGGACCTCAGACCT
ss.AC003042	<div>36550 36560 36570 36580 36590 36600</div> TCCTCTTTGTTGGGGGACTGCCTGTATACCAGAAATTAGCACACACCTGTGTGTGTATGG
ss.AC003042	<div>36610 36620 36630 36640 36650 36660</div> CCTGTAATTTAAGCCTCAATCCCCTTTGGTTTAAGTGAACCTGTCTTCCCAGAGGCCAGC
ss.AC003042	<div>36670 36680 36690 36700 36710 36720</div> CAGCCTGCTGCCCAGGGAGTGAAGCAGGGAGAAGCCCCCTGTACCTGACTAAGCCCAGGA
ss.AC003042	<div>36730 36740 36750 36760 36770 36780</div> GAGTCTTCTAGATGGCCCAGACCACTGGGACAGGGAAAGCTGATGAACAGCATGCCCAGG
ss.AC003042	<div>36790 36800 36810 36820 36830 36840</div> GCAGGTTAGATCGGGTTCCAGCCACCATGGAGGAGTCTGTGGGGGGTGGGGTGCCTAAGT
ss.AC003042	<div>36850 36860 36870 36880 36890 36900</div> AGCCCCTACTCCAACCTCTAAGTTCCATGTTGGCCTTGTTCTAGAGAGCAAGCTGAACC
ss.AC003042	<div>36910 36920 36930 36940 36950 36960</div> CTGCATCCCATATGCAGGGAGCACTGGGACGCCTACATTCATTTTCATCAACTGCATTAG
ss.AC003042	<div>36970 36980 36990 37000 37010 37020</div> GTTTCTCCAGAGAAACAGAACCAATGTGTGTGTGTTCAAGAGATTATAAGGCATTGGCTC
ss.AC003042	<div>37030 37040 37050 37060 37070 37080</div> ATGCAATGATGGAGGCGGGCAAGTCTCAAGATGTGCAGGGTGAGTCAGCAAGCTGGACGC
ss.AC003042	<div>37090 37100 37110 37120 37130 37140</div> CCAGGAGAGCCGATGGTTTCATTCCAGCCTGAGTTTGAAGGCCTGAGCACCAGGAAAACC
ss.AC003042	<div>37150 37160 37170 37180 37190 37200</div> AATGGTATCATTTCCATTCAAAGGCCAGCACGCTTGAGATCCAGGAAGAGCTGATATTTT
ss.AC003042	<div>37210 37220 37230 37240 37250 37260</div> AGGTCTAGTCTGAAGGTAGGAAGGATTCTCTGACTTGGGAGAGGTCAGACTTTTTGTTCT
ss.AC003042	<div>37270 37280 37290 37300 37310 37320</div> ATTCAGGCCCTCAACTGAATGGATGAGACCCACTCACATTAGGGGTCTGCTTGACTCAGT
ss.AC003042	<div>37330 37340 37350 37360 37370 37380</div> CTACCAATGTAAACGTTAATCTCTTCCAAAAACAGCCTCAGAGAAACACCCAGAATGTTT
ss.AC003042	<div>37390 37400 37410 37420 37430 37440</div> GACCAAACATCTGGGCAACCCATGGCCCAGTCAAGTTGATACACAAAATTAACCACCACA
	<div>37450 37460 37470 37480 37490 37500</div>

ss.AC003042	TCAAAGTCTGTATTATTGTGCGCTAGTCCTGGGGTGCAGTGTCTCTGGTTTACAGAACA
	37510 37520 37530 37540 37550 37560
ss.AC003042	TCTTTTACCGATACTCTCATTATTTTATAACTTCTGTTGAAAAGGAAGGGGGTAGAT
	37570 37580 37590 37600 37610 37620
ss.AC003042	AGGGCTGGTAGTAATGGTACTATCCCCAAGATGAGGAGGCTGAGAAGCCATCTCAGTGGA
	37630 37640 37650 37660 37670 37680
ss.AC003042	AAGCCATGGAGCCAGGACTGGAATGAGCACCTTCCGGAACCTGAGGGACAGATGAAAGCT
	37690 37700 37710 37720 37730 37740
ss.AC003042	CACCCTCACCTAAACTTTTCAGGCATGAGCTCAAAGCACAGGTGTGCATGGGAAGCAGTT
	37750 37760 37770 37780 37790 37800
ss.AC003042	TCTTGGACATGAGTGAGTGGCTCAAAGGCCACTGATTCTTGAACCTGGTCACACAATGAG
	37810 37820 37830 37840 37850 37860
ss.AC003042	ATCAACTAGTAGCTTTAAGAAATATCGGCTGGGCATGGTAGTGCACGCCTGTAATCCTAG
	37870 37880 37890 37900 37910 37920
ss.AC003042	CACTGTGGGAGGCCAAGGCGGGCAGATCACCTGAGGTCAGGGAATTTGAGACCAGCCTGG
	37930 37940 37950 37960 37970 37980
ss.AC003042	CCAACATGGAGAAACCCCATCTCTACTAAAAATACAAAACCTTAGCCGGGTGTGGTGGCAC
	37990 38000 38010 38020 38030 38040
ss.AC003042	ATACCTGTAATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAACCGCTTGAACCCAGGAGC
	38050 38060 38070 38080 38090 38100
ss.AC003042	CAGAGGTTGCAGTGAGCTGGGATTGTGCCACTGCACTCCAGTCTGGGCAACAGAGCAAGA
	38110 38120 38130 38140 38150 38160
ss.AC003042	CTCCGTCTCAAAAAAGAAAAATAAAAACCAACACATGGCTCCTTCTCCAGAGATTCTG
	38170 38180 38190 38200 38210 38220
ss.AC003042	ATTTAATCAGTCAGGTGCCTCTGGGCTTCTGAAATATTAAAAATATTCTCCTCCTTGACC
	38230 38240 38250 38260 38270 38280
ss.AC003042	CCAATGACAAGCCAAAGTGAAACATCACTACACTAGGCACTTGGCCAAGAATGAAGCAGG
	38290 38300 38310 38320 38330 38340
ss.AC003042	GATGGGTGAGAGCCTGCGTGGCAGTCAGGGACAGGGAGCTCAAGGGGGGCAGAAGCTGAT
	38350 38360 38370 38380 38390 38400
ss.AC003042	CAGTGCAGTTTATGAAGGAATTCTGTCTCTTTCTTGAGAGGAGTAACTTTGACTTTAAA
	38410 38420 38430 38440 38450 38460
ss.AC003042	AAGATCTTAGGCCAGGCGCAGTGGCTCACGCCTGTAATCCCAGCACATTGGGAGGCCGAG
	38470 38480 38490 38500 38510 38520
ss.AC003042	GCGGGTGAATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAACCCCGT
	38530 38540 38550 38560 38570 38580
ss.AC003042	CTCTATGAAAAATACAAAAAATTAGCCAGGCTTGGTGGCGGGCGCCTGTAGTCCCAGCTA
	38590 38600 38610 38620 38630 38640

ss.AC003042	CTCGGGAGGCTGAGGCAAGAGAATGGCATGAACTCGGAAGGCAGAGCTTTCAGTGAGCCG
ss.AC003042	<div>38650 38660 38670 38680 38690 38700</div> AGATCGCGCCACTGCACTCCAGCCTGGGCAACAGAGCGAGACTCCGTCTCAAAAAAAAAA
ss.AC003042	<div>38710 38720 38730 38740 38750 38760</div> AAAAAAGATCTTAGGCCCTTTTTAGGCCAGGTTACACCTGTAATGCCAGCACTTTGGGA
ss.AC003042	<div>38770 38780 38790 38800 38810 38820</div> GGCTGAGGCGGGCAGATCACCTGAGGCCAGGAGTTTGAGACCAGCTTGGCCAACACAGTG
ss.AC003042	<div>38830 38840 38850 38860 38870 38880</div> AAACCCCATCTCTACCAAAAAAAAAAATATAAAATTAGCTGCGCGTGGTGCACGCCTGTA
ss.AC003042	<div>38890 38900 38910 38920 38930 38940</div> GTCCCAGCCACTTGGAAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGCAGAGGATG
ss.AC003042	<div>38950 38960 38970 38980 38990 39000</div> CAGTGAGCCAAGATCGCGCCACTGCACTCCAGCCTGAGCGACAGAGTGAGACCCTGTCTC
ss.AC003042	<div>39010 39020 39030 39040 39050 39060</div> AAAAAAAAAGGAGCATAGGCCCTTTTTAAACAACTTTAAGTGTGCTCTAAATTGGCATT
ss.AC003042	<div>39070 39080 39090 39100 39110 39120</div> GCCATTATTAGAATTGAGACAAATCCAATGCAGATGGATTCCAGAGAAAAGTGGAGTACT
ss.AC003042	<div>39130 39140 39150 39160 39170 39180</div> ATTTATTGAGCACCTAATACATGTGAGTTCCTATTGCCCTCCATATTCTCCCAACAATCC
ss.AC003042	<div>39190 39200 39210 39220 39230 39240</div> AGGAAGGTAGGATTATTCCCCTTTCGCCCAGGAGGGCACCGAGGCCCAGGTGGGTAAGGA
ss.AC003042	<div>39250 39260 39270 39280 39290 39300</div> GCGCCCCCCCCAAGGTCACATAGCAGTCAGGATTGCAAGTTCGGGGTTGCTATCCTCCAA
ss.AC003042	<div>39310 39320 39330 39340 39350 39360</div> GCCATGCTCCAGGAGGGGAGATTTTGTCTCTTAGAAGCCATCTGGCAACGTCTGGAGAC
ss.AC003042	<div>39370 39380 39390 39400 39410 39420</div> ATTTCTGGTTTCATAATGAGGGGTCATGCTACAGGCATCTAGTGCGTATAGGTCGGGGAT
ss.AC003042	<div>39430 39440 39450 39460 39470 39480</div> TCTGCTAAACATCCTACAGTGCACAGGATGGCTCTCACAACAAAAAATTATCTGGCCCAA
ss.AC003042	<div>39490 39500 39510 39520 39530 39540</div> AATGTCAAGGGTGTGGAATTTGAGTCCACCTGCCCTAGTGGTGATTCTCAGCCTTGGCTG
ss.AC003042	<div>39550 39560 39570 39580 39590 39600</div> CACATTAGACCAATGGTGGCGCTTTCGAAAGCCGGATGCCAGGTGGCGCCACACCCATCA
ss.AC003042	<div>39610 39620 39630 39640 39650 39660</div> TGTCAGACTCTCTGGTGTGAGTGTGGGTTTTTAAAGCATGCCAGGTGGTTCCAATGTG
ss.AC003042	<div>39670 39680 39690 39700 39710 39720</div> CCACCAGGACAGAAACACTTCTATGCTCCTCACACTGCTGGCTCCTGCTGCTTTCCTGGG
	<div>39730 39740 39750 39760 39770 39780</div>

ss.AC003042	ACCCGAGGGGAGGAGTGCCAAATCTGTCTCGGTTGTACAATCAACGGCAAGCCTGCTCCC
ss.AC003042	<div>39790 39800 39810 39820 39830 39840</div> AGTTCCTCCCCTTGAGGGGAAGTGAAGTCACTCAGTCACCCGTGGGGGGCCCCCGTGGGGTGGGA
ss.AC003042	<div>39850 39860 39870 39880 39890 39900</div> GGTGTGTTGCTAATTTCCCGTCGCCTCTCATGGGGCTGCAGCCAGGAGTCTCCCCGCAAGG
ss.AC003042	<div>39910 39920 39930 39940 39950 39960</div> AGGCTGTGGAAGCTGCCTGAAGACTGGACCGAAGAGCGAGGCTGCCACCTAACGGAGGAA
ss.AC003042	<div>39970 39980 39990 40000 40010 40020</div> TTGGCCAGAATCTCCACGTGCTGAGTGATGTTTTATTTGAGCCTCACAACAACCCTGTG
ss.AC003042	<div>40030 40040 40050 40060 40070 40080</div> AGGTAGGTGCAGAGTCCCGCGGCACAGAAAGATGAGGCCTGCGCTCAAGGCCCCAGGGCG
ss.AC003042	<div>40090 40100 40110 40120 40130 40140</div> GGGCCGTGTGTGGGCCTGAGGTGCGCACTGTCTACTCCACATCAGGGCCCCGCCCTCCAC
ss.AC003042	<div>40150 40160 40170 40180 40190 40200</div> CCCCACATTCTCATACACACATTTGCCACAGGCAATGACTGGTTCAAGAGGAACGGGTC
ss.AC003042	<div>40210 40220 40230 40240 40250 40260</div> CCCTGGGCTGGGCTGCCTGCCTCTCTGCAGATGTCTAACTTTCCCTCAACTTCCAGGCA
ss.AC003042	<div>40270 40280 40290 40300 40310 40320</div> GGGCCTGGGAACAGATTCCCTCCATGCTAGGCCATCATGGCTTCCCATGGAAATTAACAA
ss.AC003042	<div>40330 40340 40350 40360 40370 40380</div> ATCACCATGTCCTACTACAGGTCCAACATCACAACAGGAAACAGCTTCCTCTGGTGTCCA
ss.AC003042	<div>40390 40400 40410 40420 40430 40440</div> CCGCAGTCCCCTTCCCCCCCCCTCAGACTGTGGTCAATAAACATGGGCCTGGTGCACACT
ss.AC003042	<div>40450 40460 40470 40480 40490 40500</div> CAGGCAGAGGCTCCCCGCACACTGGAGCCGGCGGAGGCAGGTGCGGCCGTCCCTGACTCC
ss.AC003042	<div>40510 40520 40530 40540 40550 40560</div> AGCACATGAACACTGTGGACAGTCCACGTGAGCCCTCATTTTGCCTCTCTTTCTCTGGGC
ss.AC003042	<div>40570 40580 40590 40600 40610 40620</div> CTGAAGACAGCCCTGGGTGCTGAGCCATGCTGAGCCCTTCAAGCCTGGCTGAGGGTTCTT
ss.AC003042	<div>40630 40640 40650 40660 40670 40680</div> GGGGGTCTTGAGAAAGCTGCCTTCTCTCCCCCTCTGTGGGGAAACCTTCTCTGGCTGC
ss.AC003042	<div>40690 40700 40710 40720 40730 40740</div> AAATGGAGTGAAGAAGAATTCTTGCACAGACACAAGGACAAGGGAAGAGAGGACGGAGGA
ss.AC003042	<div>40750 40760 40770 40780 40790 40800</div> GAAGGATGATGTTTAGAGACCTAGACATTGAGGCAGCCCCTCATCTCATCAACGGGATGT
ss.AC003042	<div>40810 40820 40830 40840 40850 40860</div> AATTTCCCCATTTTGTACATAAAGCAACTGAGGCACACAAACAGCCAGCAAATGGGATTA
	<div>40870 40880 40890 40900 40910 40920</div>

ss.AC003042	GAGGGCATCAAATCCCACCTGCGTGATTAGAGGGATAGAGGAAAGGGAAAGGGGAGTAGA
ss.AC003042	<div>40930 40940 40950 40960 40970 40980</div> CTCACCTGCAGCCACAGAGACGTTCAAGGACTCAAGTCCAGGAGGCAGCTGGCGCCGGGG
ss.AC003042	<div>40990 41000 41010 41020 41030 41040</div> CAGGATGGTGAGGAGAAGCTGGCAGGAGGCCTGCACCTCCTGGGATAGACCTGAGCCCTC
ss.AC003042	<div>41050 41060 41070 41080 41090 41100</div> ATTCCCTGCAGGGCGTGGGGCTGAGGGTTAGGGTTGCCAGCTGGACACCCAGTTGCTCG
ss.AC003042	<div>41110 41120 41130 41140 41150 41160</div> GGAAATGTAATCTGGGCACAAACGCAGGGACATCCACCTACCCAGCACAAGGAGAGTAGG
ss.AC003042	<div>41170 41180 41190 41200 41210 41220</div> CCGTTCCCAGAGGAAGTCCAAGCAACTCATGATGGGGATCTCGGAGGACTGGGGATCCTC
ss.AC003042	<div>41230 41240 41250 41260 41270 41280</div> TGTGCTTGGGCAGCCCACCGTGCCGGCCACGAGCCAGCCCTGCTGGGCTTTGGTCTGAAA
ss.AC003042	<div>41290 41300 41310 41320 41330 41340</div> GGGGGAAGAAGATATGTTCTAATTCCTTTTTTATTTTAAATTTTGAGATAGGGTCTTACTC
ss.AC003042	<div>41350 41360 41370 41380 41390 41400</div> TCGCTCAGGCTGGAGTGCAGTGGCACGATCACAGCTCACCGCAGCCTCAACCGCCTGGGT
ss.AC003042	<div>41410 41420 41430 41440 41450 41460</div> TCTGGTGATCCTCCACCTCAGCCTCCCAAGTAGCTGGGACTACAGGCACTCGCCACCCC
ss.AC003042	<div>41470 41480 41490 41500 41510 41520</div> ACCCGGCTAGTTTTTGCATTTTTTTTTTTTTTGGAGATGAGGTTTTGCCATGTTGCCCTGGTT
ss.AC003042	<div>41530 41540 41550 41560 41570 41580</div> GGTCTGGAACCTCCTGGCTTCAAGCGATCCTCCACCTTGGCCTCCCAGAGTGCTAGGATT
ss.AC003042	<div>41590 41600 41610 41620 41630 41640</div> ACAAGCGTCAGCCACCATGCCTGCCTCTCCTATTCTAATTCATCAAATCTTCATCAGAGG
ss.AC003042	<div>41650 41660 41670 41680 41690 41700</div> CTGTATGCAGTGGCTCAAGCCTGTAATTCAGCACTTTGGGAGGCTGAAGCAGGCAGATT
ss.AC003042	<div>41710 41720 41730 41740 41750 41760</div> ACCTGAGGTCAGGAGTTCAAACTAGCCTGGCCCAGGCACGGTGGCTCACGCCTGTAATC
ss.AC003042	<div>41770 41780 41790 41800 41810 41820</div> CCCAGCACTTTGGGAGGCCAAGGCAGGGGGATCACCTGAGGTTGGGAGTTCGAGACCAGT
ss.AC003042	<div>41830 41840 41850 41860 41870 41880</div> CTGAACAACATGGAGAAACCCCGTCTCTACTAAAAATACAAAATTAGCCGGGCATGGTGG
ss.AC003042	<div>41890 41900 41910 41920 41930 41940</div> TGCATGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCGGG
ss.AC003042	<div>41950 41960 41970 41980 41990 42000</div> AGGCAGAGGCTGCAGTCAACCGAGATTGCGCCATTGTACTCCAGCCTGGGCAGCAAGAGT
	<div>42010 42020 42030 42040 42050 42060</div>

ss.AC003042	GAAACTCCATCTCAAATTA	AAAAAAAAAAAAAAAAAAAAACCAGGCTCAGTAGCTCACGC				
ss.AC003042	42070	42080	42090	42100	42110	42120
	CTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCGGATCACCTGAGGTCAGGAGTTTGA					
ss.AC003042	42130	42140	42150	42160	42170	42180
	GACCACCCTGGCTAACATGGTGAACTCCGTCTCTACTAAAAACACACAAAAAATTAGCT					
ss.AC003042	42190	42200	42210	42220	42230	42240
	GGGTGTGGTGGCACATGCCTGTAGTCCCAGCTATTTGGGAGTCTGAGGGAGGAGAATCGC					
ss.AC003042	42250	42260	42270	42280	42290	42300
	TTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGAGCACACCACTGCCTCCAGCCTGGG					
ss.AC003042	42310	42320	42330	42340	42350	42360
	CAACAAAGCGAGACTCCACTCTGTCTCAAAAAAAAAAAAAAGACTAGCCTGAGCATCAT					
ss.AC003042	42370	42380	42390	42400	42410	42420
	GGTGAACTCTGTCTCTACTAAAAATACAAAATCAGCCTGTAATCCCAGCTACTCAGGA					
ss.AC003042	42430	42440	42450	42460	42470	42480
	GACACGAGGATCTCTTGAGACCAGGAGGCAGACATTGCAGCGAGCTAAGATTGCGCCACT					
ss.AC003042	42490	42500	42510	42520	42530	42540
	GCACTCCTGCTTGGGTGACAGAGTGAGACCCCATCTCAAAAAAAAAAAAAAATTAT					
ss.AC003042	42550	42560	42570	42580	42590	42600
	CCATCAGAGCCCTGGCCAAGGAAGAGCCAGCCTTGCCCATACATTCATTTATCTGCTGA					
ss.AC003042	42610	42620	42630	42640	42650	42660
	TCCAGTCAATTAGTCAATAGTTATTAAGCACCTAGCATGGGCTCTGTTCTAGGCACTGAG					
ss.AC003042	42670	42680	42690	42700	42710	42720
	GACAGGGCACTGAACAAAACAAAACAGACCAAATCCCAGCCTTGTTGGAAGGGCAGGTGG					
ss.AC003042	42730	42740	42750	42760	42770	42780
	GGATGGACTCACTGAGGTGACATTTGAGTGCAGACCTGAAGGAGAAGGAGGAGCACCGTG					
ss.AC003042	42790	42800	42810	42820	42830	42840
	CAGACATCTGGGGCAAGAACATTCTAGGCAGAGAGATCAGCAAGCACAGAGGCAGGTGCC					
ss.AC003042	42850	42860	42870	42880	42890	42900
	TCCCTGGCATGTTTGAGAACAGTAAGGTGGCCAGTGGGAAGAGAGGCGTCAAGACAGAAG					
ss.AC003042	42910	42920	42930	42940	42950	42960
	AAGGAACAAGAGCCACATGAGGTATGGTCTCCAGGGCTACTGGAAGGACTCTGCCTTTGA					
ss.AC003042	42970	42980	42990	43000	43010	43020
	ATCTGAGCGGTACAGAGGCTTTGAAAGGTTTGTAGCAGAGAAGTAACATGGTATGACTTC					
ss.AC003042	43030	43040	43050	43060	43070	43080
	AACAGAATCACTCTGCCTGCTGTGCTGAGAGCCAAGAGCAGAAGAAAGAGGCCAGGTGG					
ss.AC003042	43090	43100	43110	43120	43130	43140
	GAAGTTTCTGCAATAACGGTCAACAGATGATGGTGACTTGCTTGGGCCAGAGTGGTAGCA					
	43150	43160	43170	43180	43190	43200

ss.AC003042	GTGGAAACAGGCAGAAATGGTGATAATACGGAAATAACTTTAGTTAAGGATGATGCCAAG
ss.AC003042	<div>43210 43220 43230 43240 43250 43260</div> GTTTTTGACCTAAACAACCAAAGGGATGGAGTTGCTCCAGAAGGAACAAGCGCTCAGTTT
ss.AC003042	<div>43270 43280 43290 43300 43310 43320</div> TAGAAATGTTAGGTTTGAAATGCCCGCTGACAGCAAAACAACAACAATAACAACAA
ss.AC003042	<div>43330 43340 43350 43360 43370 43380</div> CTGTGCAGTAGGCAACTAGATGAGTGAATCTGGAATTCAGAACCAAGGTCCAGGCTGGAG
ss.AC003042	<div>43390 43400 43410 43420 43430 43440</div> TATACACTTGGGCGGGAATTTGAATTCAGATAGTATTTAAAGCCATGAGACTAGATGAGA
ss.AC003042	<div>43450 43460 43470 43480 43490 43500</div> CCAACAAGAAATGAACATATACAGAAAAGAGATCCAGGACCAGGTGAGGTGGCTCACGCC
ss.AC003042	<div>43510 43520 43530 43540 43550 43560</div> TGTAATCCCAGCATTTTGGGAGGCTAAGGCAGGAGGACTTCTTGAAGCCAGGAGTTTGAG
ss.AC003042	<div>43570 43580 43590 43600 43610 43620</div> ACCAGCCTGGGCAACAAAGTGAGACCTCATCTCTACAAAAAAAAAAGAAAAAGAAAAA
ss.AC003042	<div>43630 43640 43650 43660 43670 43680</div> GAAAGAAAAAATTAGGTGAGATGGTGTGCACCTGTATCTCCAATACTCAGGAGGCTGA
ss.AC003042	<div>43690 43700 43710 43720 43730 43740</div> GGTGGGAGGATGGCTTGAGCCCAGGAATTCGGAGGCTATACTGAGCTGTGATTGTGCCAC
ss.AC003042	<div>43750 43760 43770 43780 43790 43800</div> TGGACTCCAGGCTGGGCAACACAGCAAGACCCCATCTCTCTCTCTCTCTCTCTTTT
ss.AC003042	<div>43810 43820 43830 43840 43850 43860</div> TTTTTTTTTTTGGAGATAGAGTTTCACTCTTATTGCCAGGCTGGAGTGCAACGCTGTGATC
ss.AC003042	<div>43870 43880 43890 43900 43910 43920</div> TCGGCTCACTGCAACCTCCGCCTCCTGGATTCAAGCAACTCTTCTGCCTCAGCCTCCCGA
ss.AC003042	<div>43930 43940 43950 43960 43970 43980</div> GCAGCTGGGATTACAAGTGCCCGCCACCATGCCAGGTAATTTTTGTATTTTTAGTAGAG
ss.AC003042	<div>43990 44000 44010 44020 44030 44040</div> ACAGGGTTTCACCATTTTGGCCAGGTTGGTCTCGAACTCCTGACCTCAGGTGATCCACCT
ss.AC003042	<div>44050 44060 44070 44080 44090 44100</div> GCCTCAGCCTCCCAAAGTTCTAGGATTATAGGCGTGAGCCACCGTGCCTGGCCAAGACCC
ss.AC003042	<div>44110 44120 44130 44140 44150 44160</div> CATCTCTTAACAACCGCTCCCGCCAAGACCTCATCTCTTTTTTTTTTTTGTACACGTCAC
ss.AC003042	<div>44170 44180 44190 44200 44210 44220</div> TCTGTCACTCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTACCACCTCCACCTCCC
ss.AC003042	<div>44230 44240 44250 44260 44270 44280</div> GGGTTCAAGCGATTCTCCTACCTCCGCCTCCCGAGTAGCTGGGACTACAGGCACGAACCA
	<div>44290 44300 44310 44320 44330 44340</div>

ss.AC003042	CCACACCCAGCTAATTTTTTTGTATTTTTTAGTAGAGATGGTGTTCACCGTGTTAGCCAGG
ss.AC003042	44350 44360 44370 44380 44390 44400 ATGGTCTTGATCTCCTGACCTCATGATCTGCCTGCCTCAGCCTCCCAAAGTGCTGGGATT
ss.AC003042	44410 44420 44430 44440 44450 44460 ACATGCGTGAGCCATTGTGCCCAGCTGACCCCATCTCTTAACAACAACAACAAAAGAGAT
ss.AC003042	44470 44480 44490 44500 44510 44520 CCGAGGACTAAAATCTGGGAAATGCTAATGCTCGGAAGTCAGGGGGTTGAGGAAGAACCA
ss.AC003042	44530 44540 44550 44560 44570 44580 CTAAAAATGTCTCTCAGAGAGGACATGGTGAAGCAGAAGGAAAGCAGGTATAGTGTTC
ss.AC003042	44590 44600 44610 44620 44630 44640 AGGAGGAAGGAGTGGTCAACTGTGCCAGCTGCTGCAGATGGGTCAAGTCAGAAAAGAATT
ss.AC003042	44650 44660 44670 44680 44690 44700 GAGAACAGACCCTGGAATGCAGCAACATGGAGGCCACTGGTGACCTTGATGAAGCCTTTG
ss.AC003042	44710 44720 44730 44740 44750 44760 ATTCAAGTGTGAGAGGAAGAGCTGACTGGTGTGAGATCAAGAGCGTGAGAGGGGAATGTTT
ss.AC003042	44770 44780 44790 44800 44810 44820 GCTTGCATGCTGAAGAGAGTGTAAAGAGAAAAGTGGATGCTGCAGGAAGAGGAGGAAAATT
ss.AC003042	44830 44840 44850 44860 44870 44880 GCTACAGCAGTGTCTCTGAGTACGCAGGAAGGGATGGGGCCCCAGCACAGGCCCTGCTT
ss.AC003042	44890 44900 44910 44920 44930 44940 GGGGCACCTCCAGCTCTTCCACAGCAACAGGCGGATGACACTCTCCAGGTCAGATGCTGA
ss.AC003042	44950 44960 44970 44980 44990 45000 TGACAGTAGGGAGATGTGATGCCTGGAGCTTAAGTGGATGTTCTGCAGTGTCTGTGTT
ss.AC003042	45010 45020 45030 45040 45050 45060 TTCAGAAGCTACCTGTTTCAGGGGCTGGAAGTGATGAGTGGGAACCTCATCTCCTATCAGG
ss.AC003042	45070 45080 45090 45100 45110 45120 CTTGAGAGAAAGGGGCTCTCTACAAAAAGTGAAGCCAAAAATGCTTCTAGATATGTGCT
ss.AC003042	45130 45140 45150 45160 45170 45180 GTTCAATATAGTAGCCACTAGCTACATGTGGCTATTAAGCAATTGAAAGGTGGCTAATTC
ss.AC003042	45190 45200 45210 45220 45230 45240 AAATCGAGGTGTGTTGTATGTAAACATTTTTTAAAGGAATGTAAATATTTCAATTAATA
ss.AC003042	45250 45260 45270 45280 45290 45300 ATATTTTTTAAAGGCCAGGTGCGGTGGCTCATGCCCTATAATCCCAGCACTTTGGGAGGCC
ss.AC003042	45310 45320 45330 45340 45350 45360 GAGGCGAGTGGATCGCTTAAGGTCACGAGTTCAAGAACAGCCGGACCAACATAGTGAAC
ss.AC003042	45370 45380 45390 45400 45410 45420 CCCATCTAAATACAAAAAAAAAAAAATTAGCTGGGCATGGTGTGTGCTATAATCCAGTT
	45430 45440 45450 45460 45470 45480

ss.AC003042	ACTTGAAGGCTGAAGCAGGAGAATCACTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCC
ss.AC003042	<div>45490 45500 45510 45520 45530 45540</div> AATATTGCACCACTGCACTCCAGCTTGGGCAATAAGAATGAACTCTCTCAAAAAATTAA
ss.AC003042	<div>45550 45560 45570 45580 45590 45600</div> TAATATTAATAATAATTAATAATGATTACATGTTAAATTGATATTATTTGGATATACTGG
ss.AC003042	<div>45610 45620 45630 45640 45650 45660</div> ACACAATTTATTTAAAATGTCATCTCTTTACTTTTCAATGTGGCTACTAGAAAAGCTAAA
ss.AC003042	<div>45670 45680 45690 45700 45710 45720</div> ACTACCTATGTTTCTCACACCATATTTTTATTGGACAGCGTTGTTCTAGACAGGTCCCAG
ss.AC003042	<div>45730 45740 45750 45760 45770 45780</div> AGCTCTCCCCCTTCTTAAGAGGGAAATTTCTCACCTGCAGTTGGGGTGGGGGTTGGGGG
ss.AC003042	<div>45790 45800 45810 45820 45830 45840</div> GGGTATGGTCAGAGGGGATTCCATATGCAGAGCAATACTGCCTCCTTGTGTCCAGCAAGG
ss.AC003042	<div>45850 45860 45870 45880 45890 45900</div> GAAGCACAGCTGAAGACAAACGGATGGGAGAGGGGTTTCCAAGGTTTGTCTCTTGCTAGA
ss.AC003042	<div>45910 45920 45930 45940 45950 45960</div> TACTAATGGCATAAAGATCTTCTTGTTCAAACATCCTTTCAAGCTGTGCCCTATTTCGAGG
ss.AC003042	<div>45970 45980 45990 46000 46010 46020</div> AACTCAGGTCTCCTGTACGCAGCTCCCCACAGCTGAACAAAATGCATTTACTGAAGCCCG
ss.AC003042	<div>46030 46040 46050 46060 46070 46080</div> ACCTAGTAGGCAAATAGACACTGAGGCTGACTTACAGAAGAGGCAAAGTGGTGCATACCT
ss.AC003042	<div>46090 46100 46110 46120 46130 46140</div> GGGGAAGGGGTGCAGGAAAGGGTATAACGCTAGGAAGAATTCAGCTAATGCTCCATTTGC
ss.AC003042	<div>46150 46160 46170 46180 46190 46200</div> CGTTTTAAAAACTCCAGGACCCTTCCATCCCCAGAGGGATTTAGAAGGCCAAAGGAAGCG
ss.AC003042	<div>46210 46220 46230 46240 46250 46260</div> GTGCCAACATGCCCCCTTCTCTCCCTCGCCAGGGGCTAGCTTCGTCCTTGAAGAGGCT
ss.AC003042	<div>46270 46280 46290 46300 46310 46320</div> GAGCTGGGCTCACATCTGTTCCCTTCCCCTCTTGCCCCTCATTACCTGTAAAAATCCGGTG
ss.AC003042	<div>46330 46340 46350 46360 46370 46380</div> AGGTCATCAGTGGAGAACACGTCCATCACCTCCATAGCCCCCGCGCTGGACTTGCTGACT
ss.AC003042	<div>46390 46400 46410 46420 46430 46440</div> ACTGGAGTGAGCGGGCAGTGCAAGGTTTCCCCGTCCCCGCATTAGGCTGGGCCATCTC
ss.AC003042	<div>46450 46460 46470 46480 46490 46500</div> AAGCCCGGCTCCCTACCCTCCCAGGGCTCCCAAGGGCTAGGGGGATGAGAGTTCTGGGAC
ss.AC003042	<div>46510 46520 46530 46540 46550 46560</div> AGGTAAGTCTGGCTAAGGGATCACCCAAGGGCCAAGGTGCTTAGGAACTCGGCTGCGTCT
	<div>46570 46580 46590 46600 46610 46620</div>

ss.AC003042	CCAAGTTGGGGCACATAGAGAATGAGGGACGTCCGTGCCTGTTTCTCCGGCTGGTGATGA
ss.AC003042	<div>46630 46640 46650 46660 46670 46680</div> CCTTATCCACTCCGAGGAAGTGTGCGGAACGCAGCACAGCCCCAAAATTCCGGGGATCCT
ss.AC003042	<div>46690 46700 46710 46720 46730 46740</div> GGATCCCATCGAGGACGAGCCACAAGTGTGGGGTTCGTGCCTGGGCTCGCCTCCCCGG
ss.AC003042	<div>46750 46760 46770 46780 46790 46800</div> CCTCTCTCCAAGCCGGGGCCGAGCGGGCTCACCTCCATGCAGACACCCTGGTGGACCT
ss.AC003042	<div>46810 46820 46830 46840 46850 46860</div> GGTAGCGGCACATTGTGTCCAGTTTCTGCCGTCTGGGCCGAGAAGTGAATGTCCCGCG
ss.AC003042	<div>46870 46880 46890 46900 46910 46920</div> CCTCGGCCATCCGGAGCAGCTCGGCCCGCTTCCCCTGCAGCCCAGCTTTACCCGCCTGGA
ss.AC003042	<div>46930 46940 46950 46960 46970 46980</div> GCAGGAGCCGGGCCACAGAGCGGGCGGGCGGCTGCAGAGCCAGGAGACACGGGGTCATGC
ss.AC003042	<div>46990 47000 47010 47020 47030 47040</div> CAAACAGAAGCTCCAGCCGAGAGTTCGGCACCAGGTCATCCAGCAGCAAGCGGCTTAGCT
ss.AC003042	<div>47050 47060 47070 47080 47090 47100</div> CCTCCCCACCAGGCCGCTCCCCATGCCGCGCTGCATGGGAGAAATGACGGGTGACGAGGC
ss.AC003042	<div>47110 47120 47130 47140 47150 47160</div> GACCCAGGTCGCGCCCCGGACGGTCGAGAGCAATGCCATGGCGCAGCTCCCGCCAGGGA
ss.AC003042	<div>47170 47180 47190 47200 47210 47220</div> CTCGATGCCCTTGCTGCGTCCCCGGGAGCGGTAACCCGCGCCGAGTTTCGTCCCAGGC
ss.AC003042	<div>47230 47240 47250 47260 47270 47280</div> TCCCAACACCGAGGTGAAGGGTACTCGACAGCCGTCTCCGCCGAGCTCTCTCGGACAGGA
ss.AC003042	<div>47290 47300 47310 47320 47330 47340</div> ACAAACAGCCCCGATTACCCACAAGTGGACTACCGAGCTACGACCACCCGCTCCCAGGCT
ss.AC003042	<div>47350 47360 47370 47380 47390 47400</div> CCCACGTGGGTCCCTCGCTTCCGGGTTCTGGGAGCCCGCCCCCTCCCCGGCCCCCTTCCTGAC
ss.AC003042	<div>47410 47420 47430 47440 47450 47460</div> GGTGTTTTGCGCATGCGTGGCTGCCAGGCTGTCCCCACAGCGCCTCCCTCAAGGCTAGA
ss.AC003042	<div>47470 47480 47490 47500 47510 47520</div> GGAGCGGCGAGCTGAGCTGGCCGTACTACCGGCTGCGTCCTGTGTTTCCTCGAGGTCCAG
ss.AC003042	<div>47530 47540 47550 47560 47570 47580</div> GAGGCCGGGGACCGCATTACCCACGCACCAGTGAAGGGCCCTTTAAGGAGATGGGTTGG
ss.AC003042	<div>47590 47600 47610 47620 47630 47640</div> CCTTCCTGGTCAACCAATTGAGTCTTGTTGCCTCCCTCCCCACATCCCGGCGCTGGTGAT
ss.AC003042	<div>47650 47660 47670 47680 47690 47700</div> TTTTCCCAGAACTTCTACTAGCCCATCACCAGCCAGCAGGACCCCAACAGTCACTTCCT
	<div>47710 47720 47730 47740 47750 47760</div>

ss.AC003042 ATCCCGGGCCGCTGATTCTCTTCTAAGTGA CTCTGAGCCTGTCGTGTTCTCTGCTGACAA

47770 47780 47790 47800 47810 47820
ss.AC003042 GCTCACTAACGCCCCCGTCCCACAGGTAATGGCGAGACTCTTGCGCAGCACTCAGCCCCC

47830 47840 47850 47860 47870 47880
ss.AC003042 CAGCGATCCAGGAAGGCAGGAAGGAGCTGCCTCTTCAGCCCCATCTGGCTCCTTGCTCCT

47890 47900 47910 47920 47930 47940
ss.AC003042 GTGCTTAAGTTCTGAGCTGTTGCGACAGCACTGCATGCTCTTCCAGACCTCTCAGCCTTG

47950 47960 47970 47980 47990 48000
ss.AC003042 CACACCTGTCTTCGCTTTGTCAAACCTCTACATGTTTTCAAGGCCCAAACAAACCCATTC

48010 48020 48030 48040 48050 48060
ss.AC003042 CTGCTACCTAAGGTAATCCATACTCCCATGAGTGAGGCCCCCAATCCACCCACCTGGGAC

48070 48080 48090 48100 48110 48120
ss.AC003042 CTACCTGGAAGAAATTCTGAGACACAAGCACCCCTGATCACAGAGAAGGGGAAAGAATGG

48130 48140 48150 48160 48170 48180
ss.AC003042 AAAGACACTCCTGAAGCCAAGGCAGATTGGTTGCGATTTTTCTTTTTTAATGATCACCAT

ss.DNA77626.rc TTTTTTTTTTTTGGTTGCGATTTTTCTTTTTTAATGATCACCAT
10 20 30 40

48190 48200 48210 48220 48230 48240
ss.AC003042 GAAATCCACTGGGCCAGGCCCTGGTGTCTGCTGCCATAGTCAGAGTCAGAGTGGAGGGA

ss.DNA77626.rc GAAATCCACTGGGCCAGGCCCTGGTGTCTGCTGCCATAGTCAGAGTCAGAGTGGAGGGA
50 60 70 80 90 100

48250 48260 48270 48280 48290 48300
ss.AC003042 TGACCCCAAGGAGGGGACAAGAAGCCAAGACTGGGCTGGGGAGCCGAGAAGGAGATAGATA

ss.DNA77626.rc TGACCCCAAGGAGGGGACAAGAAGCCAAGACTGGGCTGGGGAGCCGAGAAGGAGATAGATA
110 120 130 140 150 160

48310 48320 48330 48340 48350 48360
ss.AC003042 AGGGGGAGAGGGTGCAGTGGGGCAGGCAGAGGAGGAAGTCTGGAGCCCTGGATAACAACA

ss.DNA77626.rc AGGGGGAGAGGGTGCAGTGGGGCAGGCAGAGGAGGAAGTCTGGAGCCCTGGATAACAACA
170 180 190 200 210 220

48370 48380 48390 48400 48410 48420
ss.AC003042 CAGATATAAGGTGAAGGCCTCCCTCTGCCACCCCAAGCCCTGAGCCACAGACGTTGAGGTG

ss.DNA77626.rc CAGATATAAGGTGAAGGCCTCCCTCTGCCACCCCAAGCCCTGAGCCACAGACGTTGAGGTG
230 240 250 260 270 280

48430 48440 48450 48460 48470 48480
ss.AC003042 CAAGAAGATGGGGATTTTGGCCACAACCTCTTCCCATGTCAAAGGGAAGACACTGAGAG

ss.DNA77626.rc CAAGAAGATGGGGATTTTGGCCACAACCTCTTCCCATGTCAAAGGGAAGACACTGAGAG
290 300 310 320 330 340

48490 48500 48510 48520 48530 48540

ss.AC003042	CAGACAAAGGCCAAGTGCCCAGGGGCACAAGAACAAGTTAACAAGTAAAACAATTAGGGA
ss.DNA77626.rc	*****
	350 360 370 380 390 400
ss.AC003042	48550 48560 48570 48580 48590 48600
ss.DNA77626.rc	CACCACCTCCTTTCCCCAGCCCATTTTTCACATTTACAAGCAATTGACAAGATG

	410 420 430 440 450 460
ss.AC003042	48610 48620 48630 48640 48650 48660
ss.DNA77626.rc	ATATAAAAATCTCAAACAAATTTTCTAGCCCCTGGTCGGGGTGTGGACAGGAAGTGGTAT

	470 480 490 500 510 520
ss.AC003042	48670 48680 48690 48700 48710 48720
ss.DNA77626.rc	CCCGTGATCCAGAAATCAACACCTAAAATCCAGAGGCAGGAGGCAAGCCATGAAGGGTGG

	530 540 550 560 570 580
ss.AC003042	48730 48740 48750 48760 48770 48780
ss.DNA77626.rc	GGAGGGAAGGAGGAGCTCCCACAGTCACTAGGTCACCTGCTCCGTGGGCCTCATCTGGAT

	590 600 610 620 630 640
ss.AC003042	48790 48800 48810 48820 48830 48840
ss.DNA77626.rc	GTCTCCAATCTGTGGAAGGTACAAGGCATGAGGCAGCTGTGACACTCTCCCCTGGCCCTG

	650
ss.AC003042	48850 48860 48870 48880 48890 48900
ss.DNA77626.rc	CAGGGCTCCCTGCTCCCCCTCTGTTGGGTTCCCTCCAGTGAGTAGACAGTCA

ss.AC003042	48910 48920 48930 48940 48950 48960
ss.DNA77626.rc	GGGCCAGACTCACCTGGATGTGTGCGGGGGTGTGAGGACGTAGATAACAGCCTCGGCCA

	-----CTGGATGTGTGCGGGGGTGTGAGGACGTAGATAACAGCCTCGGCCA
	660 670 680 690 700
ss.AC003042	48970 48980 48990 49000 49010 49020
ss.DNA77626.rc	CATCCTCGGGTTTGTAGACACTGAGAGCACCAGGGGAATGGGTTGAGACAAGGACAGAATG

	CATCCTCGGGTTTGTAGACA-----
	710
ss.AC003042	49030 49040 49050 49060 49070 49080
ss.DNA77626.rc	GACTCAAATTCCCTCCCACCACTGAGCTTCTCTGTGGCATCCACACATCCACCCCAACCC

ss.AC003042	49090	49100	49110	49120	49130	49140
	TCCAGGAGGAGCCACAAAGGCTGGAAGAGTGGAGTCTGAAGGCCGAGCTTCCCTCTGCCT					
ss.DNA77626.rc	-----					
ss.AC003042	49150	49160	49170	49180	49190	49200
	TCATTTAGGGAGTCAGTGGCTTCACCAGGCTCAGAGGGAGGCCCCACCTTCATTTGCTCA					
ss.DNA77626.rc	-----CTTCATTTGCTCA					
	720	730				
ss.AC003042	49210	49220	49230	49240	49250	49260
	TAGGTGGCAGCTGCCTTCTCAGGGTCCTTGTCGTGGAGTTTGAAGGCGAATTGTGTCTCC					
ss.DNA77626.rc	*****					
	TAGGTGGCAGCTGCCTTCTCAGGGTCCTTGTCGTGGAGTTTGAAGGCGAATTGTGTCTCC					
	740	750	760	770	780	790
ss.AC003042	49270	49280	49290	49300	49310	49320
	ACCACACCTGGAGAGATGCACTGGGCCAACAGAGAGGGCCTTCTCAGGGGCTGAGCTTTG					
ss.DNA77626.rc	*****					
	ACCACACCTGGAGAGATGCA-----					
	800	810				
ss.AC003042	49330	49340	49350	49360	49370	49380
	CCAGGTCTTGGGGAGGTTCGAGGGGAGAGGATGGAGGCCACAGAACCCAGCTTCACAGTG					
ss.DNA77626.rc	-----					
ss.AC003042	49390	49400	49410	49420	49430	49440
	ATGGCTGCCTGATATCCGGCAGCGCCTCCTCCCTCCGAAGCTGCCACTGGCAGTGACCA					
ss.DNA77626.rc	-----					
ss.AC003042	49450	49460	49470	49480	49490	49500
	CAATGATACCTACCATCTACAGAGCCTTTCCTATATGTCAGGTAAACGTTTACAAAAA					
ss.DNA77626.rc	-----					
ss.AC003042	49510	49520	49530	49540	49550	49560
	GTGTCCCTGAAAAGCTCATCATCTCCTTTTCACAAGTGAGAAGGCCGAGGCTTAGGGAGG					
ss.DNA77626.rc	-----					
ss.AC003042	49570	49580	49590	49600	49610	49620
	TTCAGTGACTCGCTCACGATCATGCGGCCTTCAAGAGAAGAGCCCAGAGTCCCGGTTTC					
ss.DNA77626.rc	-----					
	49630	49640	49650	49660	49670	49680

ss.AC003042	AGCCACTGTGCACCTGGTTTCCCACAGTCCCTTGCTTTCCCTCAGGTCAGCCCCCTCCCA
ss.DNA77626.rc	-----
ss.AC003042	<div> <div>49690</div> <div>49700</div> <div>49710</div> <div>49720</div> <div>49730</div> <div>49740</div> </div> GCTCAAAGTCTAAGTCTGGTCGTTGGCTCCTGGATCAGTGAAATGAGGAAATGAAGGGCT
ss.DNA77626.rc	-----
ss.AC003042	<div> <div>49750</div> <div>49760</div> <div>49770</div> <div>49780</div> <div>49790</div> <div>49800</div> </div> GCATAGGGCCATGCCTGGAGCAGCAGCACCCAGTTCTGTGCCCAGTCCACTCCCAGGAGC
ss.DNA77626.rc	-----
ss.AC003042	<div> <div>49810</div> <div>49820</div> <div>49830</div> <div>49840</div> <div>49850</div> <div>49860</div> </div> TCTGAGCGGCACATTCTGAACATGGGCTTCCTGAACGGTGTGTGTGGGTGGGGAGGGCCT
ss.DNA77626.rc	-----
ss.AC003042	<div> <div>49870</div> <div>49880</div> <div>49890</div> <div>49900</div> <div>49910</div> <div>49920</div> </div> GCGCCACCCTGTGCCCACCAGGGCTAGGCCACAGCCTCACCGTGGCTCGGATGTGGGTCT
ss.DNA77626.rc	-----CGTGGCTCGGATGTGGGTCT 820 830
ss.AC003042	<div> <div>49930</div> <div>49940</div> <div>49950</div> <div>49960</div> <div>49970</div> <div>49980</div> </div> GGGCCTCCCGAAGCTCTTGCCTCAGTCCCTCTGTCAGCGCAGTGACGGCATACTTGGTGG
ss.DNA77626.rc	GGGCCTCCCGAAGCTCTTGCCTCAGTCCCTCTGTCAGCGCAGTGACGGCATACTTGGTGG 840 850 860 870 880 890
ss.AC003042	<div> <div>49990</div> <div>50000</div> <div>50010</div> <div>50020</div> <div>50030</div> <div>50040</div> </div> CACTATAGAAGTGGGTCACAGACAGGGGTAACACTCGGTGGCCAGACATGCTGGGTGGGG
ss.DNA77626.rc	CACTATAGAAGTGGGTCACAGACAGGGGTAACACTCGGTGGCCAGACATG----- 900 910 920 930 940
ss.AC003042	<div> <div>50050</div> <div>50060</div> <div>50070</div> <div>50080</div> <div>50090</div> <div>50100</div> </div> AGAGGAAGGGGAAAGAGGAGAGAATGAAGTTCCAGGGAGACCAGTGGTGCTCCTGCCGTA
ss.DNA77626.rc	-----
ss.AC003042	<div> <div>50110</div> <div>50120</div> <div>50130</div> <div>50140</div> <div>50150</div> <div>50160</div> </div> CCCGTCCAGCCCCACCACCCAGATGCCCATCGGGAAGACTTCTAAAGGGGACCTCTACTG
ss.DNA77626.rc	-----
ss.AC003042	<div> <div>50170</div> <div>50180</div> <div>50190</div> <div>50200</div> <div>50210</div> <div>50220</div> </div> GCCATCCTACAGCTCACTAATCTAATTTTGGTTATTCAAACAGCTTTGGAAAACCCCTCCT
ss.DNA77626.rc	-----

ss.AC003042	50230	50240	50250	50260	50270	50280
	TTTCCTGGAACATCATCCCTAAGCTGACGACAGAATGCACTCTCCTGGTGGTGCAGAAATGT					
ss.DNA77626.rc	-----					
ss.AC003042	50290	50300	50310	50320	50330	50340
	CAGAATTCTCTCCATCTAATCTGTATGTTCACTGATACGGTTCTATTGGGACATCTCAAG					
ss.DNA77626.rc	-----					
ss.AC003042	50350	50360	50370	50380	50390	50400
	GCAGGTAGAGGCCATGTCCCCCTCAGACTGGGGCTCCCCAGTGGCAGACACTGTACATA					
ss.DNA77626.rc	-----					
ss.AC003042	50410	50420	50430	50440	50450	50460
	GTACTCTTTGTGCCATGAGGTGGGGTTCATCCCCAGGCCTGAGGAATCGAGGCACTTAGT					
ss.DNA77626.rc	-----					
ss.AC003042	50470	50480	50490	50500	50510	50520
	CCCAGGAGAGGCCCCAGGCTTCAGCTGTAGAGGAAGGGGCTAAGCTGCCCATTCCAGCC					
ss.DNA77626.rc	-----					
ss.AC003042	50530	50540	50550	50560	50570	50580
	AACCAGGGGCTGGTACTTGACAACATTATTCTTTCCCTCACCATAATTGTGCCATTCCAGG					
ss.DNA77626.rc	-----					
ss.AC003042	50590	50600	50610	50620	50630	50640
	TATTAAATCTGTATTTTCCCACCAAGGAACTGAGGTCCAAAGAGGTCAGGTGAGCTGCA					
ss.DNA77626.rc	-----					
ss.AC003042	50650	50660	50670	50680	50690	50700
	GCACATTACCCAGCCTGGTGGGTGAGTGGTACCCATTGGCCACCTGCCCTCACCTATTGA					
ss.DNA77626.rc	-----CTATTGA					
ss.AC003042	50710	50720	50730	50740	50750	50760
	TGTTAATGATGTGCCCATCGTCCACATTCCGCTCCTTCATGGACTGGTAGGCTTCCCGTG					
ss.DNA77626.rc	*****					
	950	960	970	980	990	1000
	50770	50780	50790	50800	50810	50820

ss.AC003042	TGCAGATGCTGAGGGCCAGCACGTTACCTGCAGGCCAGGGAGGGCAATGAGGTGTCTCC

ss.DNA77626.rc	TGCAGATGCTGAGGGCCAGCACGTT-----
	1010 1020 1030
ss.AC003042	50830 50840 50850 50860 50870 50880
	ACTCCGGCCCCAACTGAGCAAGTGATGGAGCCACAGAATGCTAGGGGGGAAGGGGGCAGTG
ss.DNA77626.rc	-----
ss.AC003042	50890 50900 50910 50920 50930 50940
	TGGCATTCCAAAACAGTGTCCAGGTCCCCCGGAGACCAGCCACAGGCACAGAGCATCTT
ss.DNA77626.rc	-----
ss.AC003042	50950 50960 50970 50980 50990 51000
	GTCTTCTACACGAGATGCCCCCTCTCCCTAAAGCCGCAACCCCCAGTTGATAACAGAGGTA
ss.DNA77626.rc	-----
ss.AC003042	51010 51020 51030 51040 51050 51060
	GCTCCTCACCTGGCTGACCCCCCAAGTTCCTGCAAACAAGAATGGAAACCCTTCAAACCC
ss.DNA77626.rc	-----
ss.AC003042	51070 51080 51090 51100 51110 51120
	ACTCCTGACCCAGGAGACTCTGTCTTGGCCATCTCCTCTATGAACAGTAGCACAGACCCT
ss.DNA77626.rc	-----
ss.AC003042	51130 51140 51150 51160 51170 51180
	CTAATTCCATAGGGAATCATTTCATTCTTCCCCCAAATACCCTACTCTTCTCTTCTCT
ss.DNA77626.rc	-----
ss.AC003042	51190 51200 51210 51220 51230 51240
	GTGACAGTCTCTGGCCCTGCTCCCTCCTAAACTGCTCAAAATCCTTACCAAAATGGCTTA
ss.DNA77626.rc	-----
ss.AC003042	51250 51260 51270 51280 51290 51300
	CAAATCTCTCTCCTCCGGCACACAGCCTAGCCTCTCCCTACCTTCTCAGCTACTCTCTG
ss.DNA77626.rc	-----
ss.AC003042	51310 51320 51330 51340 51350 51360
	CTCCTTCCCCATCCCCTCCCTTGAGATGAGTGGAGAAGAGAAGGCCTGACCCTCCTTTCT
ss.DNA77626.rc	-----

ss.AC003042	51370	51380	51390	51400	51410	51420
	ATGCCTTCCTTTAACGTGGGTTCATCTACAAGACTAGGCACGGAGACTCTAGAGGGTCA					
ss.DNA77626.rc	-----					
ss.AC003042	51430	51440	51450	51460	51470	51480
	GGTAACTTGCCACTCCTACTCCCTCTGGCAGAGGTGACCCCCACATCCCCACCCTTCAGG					
ss.DNA77626.rc	-----					
ss.AC003042	51490	51500	51510	51520	51530	51540
	GAACAGAGGTCTGAAGGCGTGTCTGCTGTAAAGCGCCTACACTGCCCCACCCGTTGGCCC					
ss.DNA77626.rc	-----					
ss.AC003042	51550	51560	51570	51580	51590	51600
	CACTCATTAGCCTCACCCGGAGGACAAGCAGAGATAAAGCTTTCAGCAGGTCCTCAGGCC					
ss.DNA77626.rc	-----					
ss.AC003042	51610	51620	51630	51640	51650	51660
	TCTCCTCTTAAGAAGAGAGGGAACCAGCAGGAGATTAGATGTTTCTCTTAATCAGGTGGC					
ss.DNA77626.rc	-----					
ss.AC003042	51670	51680	51690	51700	51710	51720
	AGAGCCTGCCATGAGGAACAGAACACCTTTGGTGTGAACCTGTCTTGGTGTTCATGGCAG					
ss.DNA77626.rc	-----					
ss.AC003042	51730	51740	51750	51760	51770	51780
	TAGGAAGAGATGGGTGCCAGGACAGGGAGGTTTCCAGCCGTGTTTCTCATCTTCTTGGCA					
ss.DNA77626.rc	-----					
ss.AC003042	51790	51800	51810	51820	51830	51840
	ATGTGGGCTTGTGAGGCAGAGAACTCAGCCCCTGGCAGGTAGAGTGGGAGAAAATAGATCC					
ss.DNA77626.rc	-----					
ss.AC003042	51850	51860	51870	51880	51890	51900
	CCTGGGACCAGGTGAGTAAATCTCCCAGGTCTAGGGTATCAGGGGCAGGGAAAGAGAAGA					
ss.DNA77626.rc	-----					
	51910	51920	51930	51940	51950	51960

ss.AC003042 TGCCTCATAGGATGATCCTAATAGACTCAGATAATGTTCAAGCTGAAAGGAGCTGTAGGA

ss.DNA77626.rc -----

51970 51980 51990 52000 52010 52020
ss.AC003042 ATTTAATGTAAGTCCCTCATTTTACAGATGGGCGAGTTGAGGTCCAGGTTTAGAGACCCA

ss.DNA77626.rc -----

52030 52040 52050 52060 52070 52080
ss.AC003042 TGTGCTGTGGGTGAGGACCATGGCTCTGATCTCCAAGAAGGCTGAGGGCTTCATTTTCAT

ss.DNA77626.rc -----

52090 52100 52110 52120 52130 52140
ss.AC003042 GGCTTCATTTCCAGGCCCAAGCATCTGTGAGGTGCTAAGTCTACTGTCAGCAGATGGGAA

ss.DNA77626.rc -----

52150 52160 52170 52180 52190 52200
ss.AC003042 AGGATTGTGGGGAGAAAAGAACACCCCATTCACACACTGCTTTCAACTTCTCAGGATACT

ss.DNA77626.rc -----

52210 52220 52230 52240 52250 52260
ss.AC003042 TTTATACCCTACTATCACCCCATCATACCATCCAGAAGTTGAAAACCCATGTCCTGAAAG

ss.DNA77626.rc -----

52270 52280 52290 52300 52310 52320
ss.AC003042 TTGGGTTTGGCCTGTGCACAGTTTCAAACATTTTAAAAACCCTTCCAACATGTACTGGA

ss.DNA77626.rc -----

52330 52340 52350 52360 52370 52380
ss.AC003042 AAGTTTCATTTATTCAATAACTATCTTTTCAGTGCTTATGGGATCAAGCCATACCAGAGA

ss.DNA77626.rc -----

52390 52400 52410 52420 52430 52440
ss.AC003042 ATAAAACAGATAAAATACTTGCCCTCATGGAGCTGTCATTTTAGTGAATGGGAGTGGGGG

ss.DNA77626.rc -----

52450 52460 52470 52480 52490 52500
ss.AC003042 GGTGTCACATAAAATCAGACTCCCCACTTCTCTCAAAGAAATCATAAGATCAGCTGGGCG

ss.DNA77626.rc -----

52510 52520 52530 52540 52550 52560
ss.AC003042 TGGTGGCTCACACCTGTAATCCCAGCACTCTGGGAGACCAAGGCAGGCGGATCACGAGGT

ss.DNA77626.rc -----

52570 52580 52590 52600 52610 52620
ss.AC003042 TAGGCGATACAGACCATCCTGGCCAACATGATGAAACCCCATCTCTACTAAATACAAAAA

ss.DNA77626.rc -----

52630 52640 52650 52660 52670 52680
ss.AC003042 AAATTAGCTGGGCATGGTGGTGGCCGCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAG

ss.DNA77626.rc -----

52690 52700 52710 52720 52730 52740
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ss.DNA77626.rc -----

52750 52760 52770 52780 52790 52800
ss.AC003042 CCAGCCTGGTAACTACAGAGCAAGACTTCGCCTCAAAAAAAAAAAAAATTTTCATCAAATC

ss.DNA77626.rc -----

52810 52820 52830 52840 52850 52860
ss.AC003042 AGGCCACACTGGGCCCACACCACCATAGAGCAACTATGCAGGATTTGAGCAGTGGCTGTG

ss.DNA77626.rc -----

52870 52880 52890 52900 52910 52920
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ss.DNA77626.rc -----

52930 52940 52950 52960 52970 52980
ss.AC003042 GCCCCAGGGGACATTGGAGCTGTGACCCCAAGATATTGATGATAGAGGTGTGTTTCATCCCA

ss.DNA77626.rc -----

52990 53000 53010 53020 53030 53040
ss.AC003042 ATTAATTGTGACAAGACTGAAGCTCAAGGAAGGTAACCAACCTGCCTAAAGTCACATAGT

ss.DNA77626.rc -----

53050 53060 53070 53080 53090 53100

ss.AC003042	TACTAGTGAGGCTAGGTAAGAATATCATCACTTGTCTCTCTCTTCCTTTTCTTCCCATAA
ss.DNA77626.rc	-----
ss.AC003042	53110 53120 53130 53140 53150 53160 CATCACGTTCCCAAGCACCCAGGCACAGGACTGACAAGTGGGAAACATTCAACAGGCAGC
ss.DNA77626.rc	-----
ss.AC003042	53170 53180 53190 53200 53210 53220 AGTTCTCTCCCCTAACAATCTTTCTTCTAACACAAGGAAATCACTCTAGACTTTAAGAAC
ss.DNA77626.rc	-----
ss.AC003042	53230 53240 53250 53260 53270 53280 TACCTTCAGGTCGGGCGTGGTGGCTCATGCCTGTAATCCCAGCACGTTGGGAGGCCAACA
ss.DNA77626.rc	-----
ss.AC003042	53290 53300 53310 53320 53330 53340 TGGGCAGATCACCTGAGATCAGGAGTTTGAGACCAGCCTGGCCAACAAGGTGAAACCCTG
ss.DNA77626.rc	-----
ss.AC003042	53350 53360 53370 53380 53390 53400 TCTCTACTAAAAATACAAAAAATTAGATGGGCATTGATGATGGGTGCCTGTAATTCCAG
ss.DNA77626.rc	-----
ss.AC003042	53410 53420 53430 53440 53450 53460 CTACTCAGGAGGCTCAAGCAGGAGAATCGTTTGAACCTGGGAAGCGGAAGTTGCAGTGAG
ss.DNA77626.rc	-----
ss.AC003042	53470 53480 53490 53500 53510 53520 CAGAGATCATGCCACTGCACTCCAGCCTGGGTGACAAAGCAAGACTCTATCTCAAAAAAA
ss.DNA77626.rc	-----
ss.AC003042	53530 53540 53550 53560 53570 53580 AAAAAAAAAAAAAAAAAAGAACTACCTCCAGGGGCTCAAAGAAGAGAAGAGCTGATATG
ss.DNA77626.rc	-----
ss.AC003042	53590 53600 53610 53620 53630 53640 GCCATTCATCCACTCTCTATCCCTCTGGTAGGGCAAGAAGCCAAGAGAGAGTCAAGATGC
ss.DNA77626.rc	-----

53650 53660 53670 53680 53690 53700
ss.AC003042 CCCAGGTGGGAACCCGAAGCTCCCTCTTCCTAGATGTCCCGTCCCCAGCAGCACTCTGGT

ss.DNA77626.rc -----

53710 53720 53730 53740 53750 53760
ss.AC003042 TCACAAACCCCTGGCTCCCTCTCTCCTCCCCACCCTCCACCTGGAAGATGGAGGCTTGG

ss.DNA77626.rc -----

53770 53780 53790 53800 53810 53820
ss.AC003042 AGCTCTTACATTGAACATGTCCTTCCAACCACTGGTGTGCTGAGAGCAGGGTGTTCAGG

ss.DNA77626.rc -----ACATTGAACATGTCCTTCCAACCACTGGTGTGCTGAGAGCAGGGTGTTCAGG

1040 1050 1060 1070 1080

53830 53840 53850 53860 53870 53880
ss.AC003042 CCGGGCCAAGCCAGCATTGTTGATGCAGATGTCTACACCGCTGTGCTGAGAACGGATAGC

ss.DNA77626.rc CCGGGCCAAGCCAGCATTGTTGATGCAGATGTCTACACCGCTGTGCTGAGAACGGATAGC

1090 1100 1110 1120 1130 1140

53890 53900 53910 53920 53930 53940
ss.AC003042 TGAGAACATGGAGAGGATGTCTCTTTCATTTGATAGGTCACATCTGTAGGGGATCAAAGT

ss.DNA77626.rc TGAGAACATGGAGAGGATGTCTCTTTCATTTGATAGGTCACATCTGTAGGGGATCAAAGT

1150 1160 1170 1180 1190 1200

53950 53960 53970 53980 53990 54000
ss.AC003042 CCCGGGGTAGCCTGCACTCTTACATTTCAGCAGCCAGCTCCTATGAAACCCAACAGGGGTC

ss.DNA77626.rc CCCGGGGTAGCCTGCACTCTTACATTTCAGCAGCCAGCT-----

1210 1220 1230 1240

54010 54020 54030 54040 54050 54060
ss.AC003042 TGACTGGGGTGAGCAGCTCACTCCCACGGCTCCCTAGCCAGCCTCAGACCCCGACCCCG

ss.DNA77626.rc -----

54070 54080 54090 54100 54110 54120
ss.AC003042 TCACACTCATAAAACATGCTCCTTTGGCAGCTGACTTTTCAGCCACGAAGATGTTGGACTG

ss.DNA77626.rc -----

54130 54140 54150 54160 54170 54180
ss.AC003042 CCCATCCCCTAAGTCTGTCTCTTTGGTCAAAGTCTAAGGGATGACAGTGCTCCCCGAGT

ss.DNA77626.rc -----

54190 54200 54210 54220 54230 54240

ss.AC003042	GATGAAGGGAAAAGGCTGTTATCAATGGAGAAACCTCACTATAAACTCAAGTCCTGGCTG
ss.DNA77626.rc	-----
ss.AC003042	54250 54260 54270 54280 54290 54300 GGCGTGGTGGCTCATGCCTGTAATCCCAACACTTTGGAAGGCCAAGGCGGGTGGACCAGT
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ss.AC003042	57010 57020 57030 57040 57050 57060 GCCCCGCCGCTCTCCTGCCGCCGCCGCCGACCTGCTTGGGTCCGATCCGCGCCTAGACCC
ss.DNA77626.rc	GCCCCGCCGCTCTCCTGCCGCCGCCGCCGACCTGCTTGGGTCCGATCCGCG

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	TATCCAGTCGGAGGCCGCCGCGGCCCGGCCCGCCCTTCCGCCCTCTGCCCCGCC					
ss.AC003042	57190	57200	57210	57220	57230	57240
	CCGGCGTAGGGAAACCGGGCTGCGCGGGAGCGTCCTGGCAGCTGGCGGCGCCGCTTCCCC					
ss.AC003042	57250	57260	57270	57280	57290	57300
	AGTGAGCGCTGCCCTTTGGGGTCAGGGAAACCGAGGTTTAGCGGGGAGGTTCTTCAGCC					
ss.AC003042	57310	57320	57330	57340	57350	57360
	CCAAGGGCGCATACTGAAGCGTCCCGCTTAGTCTCCCTTCTCTACTCTGAACCCTAATG					
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	CCCGCCGGTGGCTGATGGGAAGGGATTCCGCCCAGAAAACGCCGAGTGTCTCCGCCATCA					
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	ACGGAGAACTGAAATACTCCTAAGTACACGTGTACTGGGGTATTCTGTCCCTAAATGGCC					
ss.AC003042	57610	57620	57630	57640	57650	57660
	CACGTGTCTAACTGCCCTAGACCCCCACGCTTACCCCTACCCCACTGTAGCAAATGTAT					
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	CATGATATATGCCAAAGATTAACAGTATCTAACATTTGCTGCTTATGGTGTAGCAGGC					
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	ATTTTAAATATAGTAATACTACACAACCGCGCTGAGATGGCACATATTAGTATCTTA					
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	ATTTTAAAGATGAGTATACTGACGTGGTGAAGCATGGTTTGGACCACAGGCAGTCCAGTC					
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	TTTGTTCAGAGTAGAGCTCGCTTACTAAAAGTGCTGAAAACCTGCGTACTTAATATAGC					
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	CATTCTCTTAAAGAAAAAGCATCTTTGAATAACCACCTGACTCCCTTCCAGCAAGCAATG					
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ss.AC003042	58090	58100	58110	58120	58130	58140
	TTTGGCCCCAATGGCAAAGATTAAAACTAAACTAAATCAGCCTTTCTTTTAGGGATCTC					
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ss.AC003042	58210 58220 58230 58240 58250 58260 TGGGAGACCCACAGTCATTTTTTAGATTCTGGGATGAAATCAAAAAGGGTCCAAGAGGAG
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ss.AC003042	<div>63130 63140 63150 63160 63170 63180</div> ATCAAGTGAGAGTTACTATTAACATACCAATAAGTATATTAGGACAAAGAGTGAACCTT
ss.AC003042	<div>63190 63200 63210 63220 63230 63240</div> TGGGGACCACAGAAAAATCTCATAATTAATGGCTTATTTAAAGTAGAACATTTCCAATGA
ss.AC003042	<div>63250 63260 63270 63280 63290 63300</div> AGGATTTTTTTTTTAAGTAGAAAGTAAATTAATAATGAAAATATGATTAGGAATTTACC
ss.AC003042	<div>63310 63320 63330 63340 63350 63360</div> ATTTTTCGTTTTTGTCAAAAATAAGTCAAAGAACATAAAGAAAAAGGAAATATTAAGTAT
ss.AC003042	<div>63370 63380 63390 63400 63410 63420</div> CTGACTAAATTATATGATATTCTTGGAACATAAAGCAGTTTTTAAATTTCTAGCTCACAG
ss.AC003042	<div>63430 63440 63450 63460 63470 63480</div> AATCTCTAAAAGCTCTTACATTTAACAGTAAGAAAGAATAGAGTTAAGAGTTCATTTTAA
ss.AC003042	<div>63490 63500 63510 63520 63530 63540</div> AAAGAAATTATTTACTTACCTTTCTTTATTTTAGGGGACCCCAAAGATTGCCACTGCTA
ss.AC003042	<div>63550 63560 63570 63580 63590 63600</div> GGACAGGTACATGATGTATTTTCATTGGTAACAATTACTTCTACACAAGTATTACCATCT
ss.AC003042	<div>63610 63620 63630 63640 63650 63660</div> TCAGTGCTGCCACAGGCTTTGCAGCTGCTATTTTCTATGAAGTCTGTTTCCTTTAAGGAT
ss.AC003042	<div>63670 63680 63690 63700 63710 63720</div> CAACATTAAGAGAGAGTCAAGAGCTTTACTCCATAACAGCTACATTTTATTCCTTAGATC
ss.AC003042	<div>63730 63740 63750 63760 63770 63780</div> AAAACATTTTTCATCCTAATAGTAAGATGTGGCATTTCCTACTGTACTGACATTTTACTG
ss.AC003042	<div>63790 63800 63810 63820 63830 63840</div> ACAGTACAAAAGTAATGGTGGGTAAAGATATTAGTCCTTAGCACAAATCAAGACAGTACT
	<div>63850 63860 63870 63880 63890 63900</div>

ss.AC003042	AACCAAAGTGTGCTAAGAATCACTGTATTCTTCAACTGTCAAGCGCTCTCACAAAAGAT
ss.AC003042	63910 63920 63930 63940 63950 63960 ATTTCACTTATGAATGTCTCTGAGGAAGCTGTAAAAATATTAATTGTATCAGATATCAAC
ss.AC003042	63970 63980 63990 64000 64010 64020 CACAAATACATATACTTTTTCTTTTTTTTTTTTTTTTGGAGTACGGTCTCCCTCTGTCACT
ss.AC003042	64030 64040 64050 64060 64070 64080 TAGGCTAGAGTACAGTCATACAATCATGGCTTACTGCAGCCTCAAACCTCTGGGCTCAAG
ss.AC003042	64090 64100 64110 64120 64130 64140 CAATCCTTCTGCCTCAGCCTCTCAAGTAGCTAGGACTACAGAAGCACACCAGGCCTA
ss.AC003042	64150 64160 64170 64180 64190 64200 ATTTTTTTATTCTTTGTAGAGACAGGGTTTCGTTATGTTGCCAGGCTAGTCTTGAAC
ss.AC003042	64210 64220 64230 64240 64250 64260 CTTGAACCTCTGGCCTTAAGCAATCCTTCTGCCATGGCTTCCCAAAGTGCTAGGATTACA
ss.AC003042	64270 64280 64290 64300 64310 64320 GGCATGAGCCTCCACGCCCTGTCAACAGAAATCTTTTTGACAGTCTATGTGGGGCCAGGT
ss.AC003042	64330 64340 64350 64360 64370 64380 GCAGTGGCTCATGCCTGTAATCCCAGCACTATGGGCAGCTGAAGCAGGTGGATCACTTGA
ss.AC003042	64390 64400 64410 64420 64430 64440 GGTCAGGAGTTCAAAACCAGCCTAGCCAAGATGGTGAGACCCCGTCTCTACTAAAATAC
ss.AC003042	64450 64460 64470 64480 64490 64500 AAAAATTAGCCGGGCAAGGTGGCAGGCGCATGTAATCCCAGCTACTCAGGAGGCTGAGGC
ss.AC003042	64510 64520 64530 64540 64550 64560 AGGAGAATTGCTTGAACACGGACGGCAGAGCCTGCAGTGAGCCAAGATCACACCACCGCA
ss.AC003042	64570 64580 64590 64600 64610 64620 CTCCACTGTGGGCGACAGAGTGAGACTCCGTCTCAAAAAAAAAAAGTATGTGACAAATG
ss.AC003042	64630 64640 64650 64660 64670 64680 GGAAGTATGCTTAAAGCATTCTATTGCAGCTGTCTCAAGGAAACGTACTTGTGCCACTT
ss.AC003042	64690 64700 64710 64720 64730 64740 TTTGAGGTGCAAGCTGAACCTTTTTCTGGAACATCAAGTTCACTTGAACGAATAAATGA
ss.AC003042	64750 64760 64770 64780 64790 64800 GAGACAACTGAGAGACTTGATATTTAGCAGGCATTTTCTCAAAAATGAATGAAGTCAA
ss.AC003042	64810 64820 64830 64840 64850 64860 TCTGTTACTTCAAAGGAAACAATGAACAACAACGTGTTGTCAATGACAAAACCTCAACATT
ss.AC003042	64870 64880 64890 64900 64910 64920 GAAACAACAATCAGAATTTTGGCCTTGCAACCAGCAGTGCTATGAACCTGAAGCTTCCTA
ss.AC003042	64930 64940 64950 64960 64970 64980 ATACTTGGACTTTTCTGACCTGCATAATTCAAGTGAACCTTGAAATAAATTCCAATGCATG
	64990 65000 65010 65020 65030 65040

ss.AC003042	ATGTTACAAAACAATGCATGAGTAAAAGATCTATTCAAAGTCCAATATAGTCCAACGGAT
	65050 65060 65070 65080 65090 65100
ss.AC003042	TCTAATTTAACAGAGTACAAAAGGTCATTGATAAGGTGCCAGATTCCATATTGCAATGA
	65110 65120 65130 65140 65150 65160
ss.AC003042	ATCTTTTAGAACTACCACTGGTCAAAGTGTAGTATTGAAGAATATCCACAACATATCTGA
	65170 65180 65190 65200 65210 65220
ss.AC003042	AAAGGTTTATATTAAAATACTGCTCCCAGCCAGGCACAGTGGCTTATTCTGTAAATCCCA
	65230 65240 65250 65260 65270 65280
ss.AC003042	GCACTTTGGGAGGCAGAAGCGGGCAGACTGCCTAAGCTCAGGAGTTCGAGACCAGCCTGG
	65290 65300 65310 65320 65330 65340
ss.AC003042	GCAACAAGGCAAAACCCCATCTCTACTAAAAATACAAAAAAATTAGCCGGGCATGGTG
	65350 65360 65370 65380 65390 65400
ss.AC003042	GTAGGCGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCACAAAATCGCTTGAACCCAG
	65410 65420 65430 65440 65450 65460
ss.AC003042	GAGGAGGAAGTTACGGTGAACCAAGATTGTGCCACTGCAATCCAGCATGGGTGACAGAGC
	65470 65480 65490 65500 65510 65520
ss.AC003042	AAGACTCTGCTCCAAAATAAAATACTTTTCTACCATATAATATCTGTGTGAGACTAGAC
	65530 65540 65550 65560 65570 65580
ss.AC003042	TTTCTTCATATGCTTCAACCAAGCCAATAAATGGAAACAGATTGAATGCAGAAGCAGATA
	65590 65600 65610 65620 65630 65640
ss.AC003042	TAAGAATCTAGTATATTCCGTCAGGCGCGGTGGCTCACACCTGTAATCCCAGCACTTTGG
	65650 65660 65670 65680 65690 65700
ss.AC003042	GAGGCTGAGGCGGGCGGATCACGAGGTCAAGAGATCGAGGCCATCCTGGCCAACATGGTG
	65710 65720 65730 65740 65750 65760
ss.AC003042	AAACCCTGTCTCTACTAAAAATACAAAAATTAGCCGGGCATGGTGGCACACGCCTGTAGC
	65770 65780 65790 65800 65810 65820
ss.AC003042	CCCAGCTACTTGGGTGGCTGAGGCAGGAGAATTGCTTGAACCCGAGAGGCGGAGGTTGCA
	65830 65840 65850 65860 65870 65880
ss.AC003042	GTGAGCCGAGATCATGCCACTGCACTCCAGCCTGGCAACAGAGCGAGACTCTGTCTCAAA
	65890 65900 65910 65920 65930 65940
ss.AC003042	AAAAAAGGAATCTAGCTTATTCCTTTTAAGATGAACATTAAAGATATTTGCAAAAAATA
	65950 65960 65970 65980 65990 66000
ss.AC003042	TATATAGTATAATACCATTCTTCTCACTCTCATTTTATTAGAAAATAGTTATTTTTGAA
	66010 66020 66030 66040 66050 66060
ss.AC003042	AAAATATTTAGTTAACATTATTTTTGAAGGAGTAGCTTAAAATTTATCATTTAATTTCTA
	66070 66080 66090 66100 66110 66120
ss.AC003042	ATACAGTAAATATTGGTAAGTATAACCCACATAAAACAAAAGCTCATTGAGTACCTTAATT
	66130 66140 66150 66160 66170 66180

ss.AC003042	TTTAAGAATGTAAAGGGATCCTAAGACCAAAAACCTTGAGAACTGCTCTAGGTCATGCACA
ss.AC003042	66190 66200 66210 66220 66230 66240 GAGGTGGCTTTCTATATTTTGACTTTGATCTAATAATACATTAAAGTCAGGTAAAGAGAT
ss.AC003042	66250 66260 66270 66280 66290 66300 AACTACTCAACATTGTCTTAATAAAACATAGACATGACATTAAAATTCTGGCTTATACAG
ss.AC003042	66310 66320 66330 66340 66350 66360 ACTACAGTAGGAAAAAGCTGATATAAAAACCTGCAGGAGCTCACATCTGGAAAAGCATAG
ss.AC003042	66370 66380 66390 66400 66410 66420 TAAAAATGCCCAAATCTAGCAAAAAGCCATACAGTTAACCTCCATATCTGTGGGTGCTG
ss.AC003042	66430 66440 66450 66460 66470 66480 CATCCATAAATTCAACCAAGAATCGAAAATATTTGGGGGGGAAAAAATCAACCTGCATCT
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ss.AC003042	66670 66680 66690 66700 66710 66720 CTCAGCCTCCCAAGTAGCTGGGATTACAGGCGTGAGCCACCATGCCCAGCCTTACATAGC
ss.AC003042	66730 66740 66750 66760 66770 66780 TTTTACATTGCATTAGGTATTATAATTTAGAGATAATTTAAGAATACAAGAGGCCAGGCA
ss.AC003042	66790 66800 66810 66820 66830 66840 CGGTGGTTCATGCCTGTAATTGTAGCATTTTGGGAGGCTGAGGTGGGAGAATTGCTTGAG
ss.AC003042	66850 66860 66870 66880 66890 66900 CCCACAAGCTGGAGACCAGCCTGAACAACATGGTAAAACGCCATCTCTACAATAAATACA
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ss.AC003042	66970 66980 66990 67000 67010 67020 GGGAAGATGACATGAGCCTGGGAGATGAACGCTGCAGTGAGCCATGATTGTGCCACTGCA
ss.AC003042	67030 67040 67050 67060 67070 67080 CTCCAGTCCGGGTGACAGAGTGAGACCCTGTCTCAGAAATAAAAGTATAAGGAGGATGTG
ss.AC003042	67090 67100 67110 67120 67130 67140 CATAGACTATATGCAAATATTACACCATTTTACATCAGGGACTTGCACATCTGCAGATT
ss.AC003042	67150 67160 67170 67180 67190 67200 TGGTATCTACAGGAAGTCCCTGGAATCAAACCCACAGATACCAAGGGACGACTGTACTTT
ss.AC003042	67210 67220 67230 67240 67250 67260 TTATTTTATTAAAAAATAAAATAAAATAAATAGAGATAGAGATCTCACTATCTTGCCC
	67270 67280 67290 67300 67310 67320

ss.AC003042	AGGCTGGTCCCAAACCTCCTAGGCTCAAGTGATACCTCCACCCTGGGCCTCCCAAAGTGCT
ss.AC003042	67330 67340 67350 67360 67370 67380 GGGATCACAGGCGTGAGCCACCACACCTGGCCTGTACTTCTATCTACAAGCAATACATAC
ss.AC003042	67390 67400 67410 67420 67430 67440 ACACTTAAGAGTTGATATTAAGAAATATTACCTTCTCTTGGCTTACTTCCTTTTCATCTG
ss.AC003042	67450 67460 67470 67480 67490 67500 CTGTTTGTAAAGGAGTAGGAATATCACACACACACTTATTTTTTCGTCTATTCTTCCGTT
ss.AC003042	67510 67520 67530 67540 67550 67560 TTTGGCGTTTCTTTTCTTGCTTGAGTTCTCTTACTCGTTCCTCTTCTGAAAATTCCTCAC
ss.AC003042	67570 67580 67590 67600 67610 67620 AAAGTTGTTCCAATCTGCTAATACCCTGTACTTTTTCCACGGTCATCTATTATAAAAAATA
ss.AC003042	67630 67640 67650 67660 67670 67680 AGGTTGAGGGTGAATATTGGTCAGAACTCTTTTCTTTTTTTTTTGGAGACGGAATCTTGC
ss.AC003042	67690 67700 67710 67720 67730 67740 TCTGTGCGCCAGACTGGAGTGCAGTGGCATGATCTCAGCTCACTGCAAGCTCCACCTCCT
ss.AC003042	67750 67760 67770 67780 67790 67800 GGGTTACGCCATTCTCCTGCCTCAGCCTCCTAAGTAGCTGGGACTACAGGTGCCCGCCA
ss.AC003042	67810 67820 67830 67840 67850 67860 CCACGCGCGGCTAATTTTTTGTATTTTTTAGTAGAGACGGGGTTTACCCTGTTAGCCAG
ss.AC003042	67870 67880 67890 67900 67910 67920 GATGGTCTCGATCTCCTGACCTCGTGATCCACCGCCTCAGCCTCCCGAAGTGCTGGGAT
ss.AC003042	67930 67940 67950 67960 67970 67980 TACAGGCGTGAGCCACCGTGCCCGTCCCTTTGTTTTCTGTGGTAATATACACACTCCTA
ss.AC003042	67990 68000 68010 68020 68030 68040 TTCCAAACCAGCAAGATTCTAGTTTTAAATTTTCAGAATTTTTTTTTTTTTTGGAGACAGAG
ss.AC003042	68050 68060 68070 68080 68090 68100 TCTTGCTCCATCGCCCAGGCTGGAGTACAGTGGCACCATCTCAGTTCACTGCAACCTCTA
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ss.AC003042	68170 68180 68190 68200 68210 68220 GCGCCACCACACTGGCTGATTTTTGTATATTTAGTAGAGACAGGGTTTCGCCATCATGGC
ss.AC003042	68230 68240 68250 68260 68270 68280 CAGGTTGGTCTCGAACTCCTGGCCTCAAGTGATCCGCCACCTTGGCCTCCCAAAGTGCT
ss.AC003042	68290 68300 68310 68320 68330 68340 GGGATTACAGGCATGAGACACCATATCTGGCCTAAATTTTCAGAATTTTAACACAACAAA
ss.AC003042	68350 68360 68370 68380 68390 68400 GTAAACATACCATTTACTGACATAATGAAAAAACTATTTAACCTGATTAGATGATCTAGT
	68410 68420 68430 68440 68450 68460

ss.AC003042	CTCTGAAGGTACAAAAATACAAAGAGAAAACGAGTAAGGGCTGGGCGCCGTGGCTCATGC
ss.AC003042	68470 68480 68490 68500 68510 68520 CTGTAATCCCAGCACTTTGGGAGGCCAAGGCAGGCAGCGGATCACGAGGTCAGGAGATTG
ss.AC003042	68530 68540 68550 68560 68570 68580 AGACCATCCTAACTAACATGGTGAAACCCTGTCTCTACTAAAAATACACAAAAAATTAGC
ss.AC003042	68590 68600 68610 68620 68630 68640 CGAGCGTGGTGGCGGGCGCCTGCAGTCCCAGCTACTCGGGAGGCTGAGCCAGGAGAATGG
ss.AC003042	68650 68660 68670 68680 68690 68700 TGTGAACCCAGGAGGTGGAGCTTGCACTGAGCCGAGATCATGCCACTGCACTCCAGCCTG
ss.AC003042	68710 68720 68730 68740 68750 68760 GGTAACAGAGCGAGGCTCCGTCTCAAAAAAAAAAAAAAGAAAAGAAAAGAAAAGAAA
ss.AC003042	68770 68780 68790 68800 68810 68820 GAAAAATAGTCCTTATACCATGGCATTACACAGCATTTACTTCATACTACTGGACATTA
ss.AC003042	68830 68840 68850 68860 68870 68880 GCAGGCAAAATGAACTCACTGAAGGTTTTAACATTTCTGCTTAATCCTTGGGGGCATT
ss.AC003042	68890 68900 68910 68920 68930 68940 TAACTTTTCACTAGTTATGTGTGTTTTTTTTGTTTTGTTTTGTTTTGTTTTGTTTTG
ss.AC003042	68950 68960 68970 68980 68990 69000 AGACGGAGTTTTGTTCTTGTTGCCAGGCTGGAGTGCAGTGACGTGATCTTGGCTCACTG
ss.AC003042	69010 69020 69030 69040 69050 69060 CAACCTCCACCTCCCAGGTTGAAGCAACTCTCCTGTCTCAGCCTCCCAAGTAGCTGGATT
ss.AC003042	69070 69080 69090 69100 69110 69120 ACAGGTGCCCCGCCACCACGCCAGCTAATTTTTGTATTTTTAGTAGAGACGGGGTTTCAT
ss.AC003042	69130 69140 69150 69160 69170 69180 CATATTGGTCAGGCTGGTCTCAAACCTCCTGACCTCAGGTGATCCGCCTGCCTCGTCCTCC
ss.AC003042	69190 69200 69210 69220 69230 69240 CAAAGTGCTGGGATTACAGGCGTAAGCCACCATGCCAGCCTCACTAGTTATGTTTCATA
ss.AC003042	69250 69260 69270 69280 69290 69300 GCAGCATCTTATTAAACATCTTCAGTTTTCTACTCTGAGAAAGTCTAAAAACCAAAGCTA
ss.AC003042	69310 69320 69330 69340 69350 69360 GCAAAGTTAACAGGATTAAAAACATTTTTTTTAAATCCATCAACTTCTTCTAAATCCCAGT
ss.AC003042	69370 69380 69390 69400 69410 69420 TCCCTAGACCACCCCACTCCAACCAAAGCCATGTAACAATATCCAGCCAAATCCATGA
ss.AC003042	69430 69440 69450 69460 69470 69480 AGCTCTATCAGTGATGGACAGTCCTTTTAGGCACTGGTGGCTTACATTAAGATTCACTCC
ss.AC003042	69490 69500 69510 69520 69530 69540 AATAACGTGACTAAGCAATCTGAGATACTGGAACAGCCCACTGTTCTTACCTCAAACTC
	69550 69560 69570 69580 69590 69600

ss.AC003042	TTGCGTAAAGCATCAACACCAAGATAGAAAAGCATCTGCCATGTCTGCTCTTCTGCCCCGT
ss.AC003042	<div>69610 69620 69630 69640 69650 69660</div> AGCTTCTGCCAGATTCGATGCAGTCTTTCATAAAGATGAATTCCCAAGCAGGTCAGAACT
ss.AC003042	<div>69670 69680 69690 69700 69710 69720</div> TCTTCTTGAGCTATATCTATTGTCTTTGCATGCCTTTCTCTTCGCCTATAAAAGGGAATA
ss.AC003042	<div>69730 69740 69750 69760 69770 69780</div> ATCACACACTAATACCTTTAACTGAAACAGTAAAAGATGGATAACACAGCTGCAAGTTCA
ss.AC003042	<div>69790 69800 69810 69820 69830 69840</div> GGTTTTTAACACAATGTGCTTACCTAGTAACAAGACAGTTATACATTTACTCAACGTA
ss.AC003042	<div>69850 69860 69870 69880 69890 69900</div> TATGTTGCTATACAAGCATGCATGTCCACAACCAATGAGAAATACACATGCAAGTAGAAT
ss.AC003042	<div>69910 69920 69930 69940 69950 69960</div> TTAGTCCTCGTATTGCTAAAAATAAAGTAATTCAGGAACTGGCTCTAAAAAGATGGGTTT
ss.AC003042	<div>69970 69980 69990 70000 70010 70020</div> TAGGGCACAAAGCAATCACATAGAAGTGTCCAGCTCATAGTAGACACAACAGTTCCTTTT
ss.AC003042	<div>70030 70040 70050 70060 70070 70080</div> ACTTTCCAATTATAGCAAAACATTTTTTCCTTCTTTAGGTTTTTTGTTTTGAGGAGGAAT
ss.AC003042	<div>70090 70100 70110 70120 70130 70140</div> TGAGAAAGGCAATGCCAAAGTGATTCATCATGGGCAAGAGTCCTCCACCAGGCCAGTCTT
ss.AC003042	<div>70150 70160 70170 70180 70190 70200</div> TACAAGTGTTACAGAACTTTGGCGATAAAAAAGCCCTTTGTATTCTAGCAGAAAGTAGG
ss.AC003042	<div>70210 70220 70230 70240 70250 70260</div> CACTCAAATGAGGGTTGATACCCTAAATACAAAAGGAAATGCATTTGATTTATTCTATTA
ss.AC003042	<div>70270 70280 70290 70300 70310 70320</div> ACATCATCATCTGATTTTATTTTACAACAAAGCCAGAGATACTACTTTAGGTTTCTGTG
ss.AC003042	<div>70330 70340 70350 70360 70370 70380</div> TAGTAATAATAATATAATATACACAGTTCGTGAATTACATTCAATAAGGCATTTCTTAAT
ss.AC003042	<div>70390 70400 70410 70420 70430 70440</div> CCCCTACTGCAAAGATCTGACTTATGCAAAAACCATTAATTGTGAATAAAATTTACACATG
ss.AC003042	<div>70450 70460 70470 70480 70490 70500</div> ATAATGCATGGATAGAGGGAGAAAAATCCCTTCTAATCATTTTCAAATGAAAATGATAGT
ss.AC003042	<div>70510 70520 70530 70540 70550 70560</div> CTGTAACAATGAAAGCCAAAAAGCCTGCCTCCCTCAAGCAAGAACTAGCAGAGGACTG
ss.AC003042	<div>70570 70580 70590 70600 70610 70620</div> AACCAAACACCAGAGAACAGTTTTTCCCTATTTTCAGTCAATTAAGAAATGCATACTTA
ss.AC003042	<div>70630 70640 70650 70660 70670 70680</div> AAGAGAAGCAAAATCTTTACAGGCATACTTTAATTTATACATATATCATATGTACTGAGG
	<div>70690 70700 70710 70720 70730 70740</div>

ss.AC003042	CAGAAGGTGATGAAAATAAACTTTTCAGTAATAAAATGAAGCAAAGCGCTAGATAGCCCAT
	70750 70760 70770 70780 70790 70800
ss.AC003042	TCTAGCAAATTACATACTCATACCTCCTGCGAACTCTGGCTCAGCACGACCCAAAAGAT
	70810 70820 70830 70840 70850 70860
ss.AC003042	GTGCAATGAAGTCTGTTTCACAGCAAACATGTATGTGTCGTTTCATGTGGACAGCACC
	70870 70880 70890 70900 70910 70920
ss.AC003042	AGCCTTCATAAAGTGCAGCACAGTAGCCCTTTTCTTTGCTGCAGTCAAGTTCACCAATAA
	70930 70940 70950 70960 70970 70980
ss.AC003042	GGATATTGTATGCTCGGAGGACTTTATTTTTTGCAATCAGTGCAAAACCTGTTGAAAAGAA
	70990 71000 71010 71020 71030 71040
ss.AC003042	AAACCTTAAAATTAAGAAATGGCTGTGCAATTATTTCTTGTGGCATATAACAGTGTACTA
	71050 71060 71070 71080 71090 71100
ss.AC003042	GATGATGGCACTCTCTCCCATCTACAGCATCCAAAATAAGCCTCCATACACACATTTAAA
	71110 71120 71130 71140 71150 71160
ss.AC003042	ACATACGCACATAAGGTAAATACAAATTTAGGGATTGCATAAATACAGATAGACCTTCAT
	71170 71180 71190 71200 71210 71220
ss.AC003042	TGGCAAATTATTTTTAACTAGAGAAACACATAGCCTAAAAGAATGAGGCAGATACATAC
	71230 71240 71250 71260 71270 71280
ss.AC003042	CTATTATTTTCATAAAATGCATGCCCAGAAAAGTATTAGTTGCCAAGAAGTACATATCTC
	71290 71300 71310 71320 71330 71340
ss.AC003042	CACTTCAAAGCTATTTGCGCAGGTGAGAAATAAAACAATAGAGGCAACAAACCAATGAC
	71350 71360 71370 71380 71390 71400
ss.AC003042	TCTTGATTGGTTTGTCTCTCTCTCTCCAGTCTCTGAAAATAGATGGTCTCTTCAGCAAG
	71410 71420 71430 71440 71450 71460
ss.AC003042	GAGACCTTGACTCCAATTTCTATTACAACATTTTAATATTTCACTAGCTAAGCATTTGAG
	71470 71480 71490 71500 71510 71520
ss.AC003042	GATAGGGGTAGGGGTGGGGTGGGGAGAAGAATGGGAAAGTGGTGTGTGCATTTTTTAAT
	71530 71540 71550 71560 71570 71580
ss.AC003042	TTTCTGATTATTTCCAAAATGCCAAATCTTTCTTCCCAAAAATGCCTATTTCTCAATAA
	71590 71600 71610 71620 71630 71640
ss.AC003042	CAAACATAATATAGACAAAATATACATGGAACTGGTTTAACTTAAGTGTATAAAATGT
	71650 71660 71670 71680 71690 71700
ss.AC003042	GGCAAAAGAATAGAAGAGTTTGTGAATGTAGAGAAGGAAGAAAATTTCTTTTAGAAACCA
	71710 71720 71730 71740 71750 71760
ss.AC003042	AATATCAATCAATCAGAAAGAAATAATAGAGCCTGGTTTCTTTATCTTTGAATTCCTGGA
	71770 71780 71790 71800 71810 71820
ss.AC003042	ACAAGAAGAACTTGGTTCAGGTGGAAAAGCCAGGCTCACAATAAGAGTAAATGGCTAAGAA
	71830 71840 71850 71860 71870 71880

ss.AC003042	GATTAGTTAAGTGAAACAAGGAAATTTTGATCTCTTTGATTTAAATTCATCTCCCAGATG
ss.AC003042	71890 71900 71910 71920 71930 71940 AGCTCATCTATGCGTATGGCTTCAACTAACATGTCTATAAAGATGACTTGTGACTCTACA
ss.AC003042	71950 71960 71970 71980 71990 72000 GCTCCATTCAAATCTCTGCTATTGCCTGAGGGCCAGACCCATATCGAAAAGTGACAAGAC
ss.AC003042	72010 72020 72030 72040 72050 72060 ATGGCAGATGTCCAATAGGCAACACCTTAAATTCAGTGTCCAAGGGTAATGCTGTTCTAT
ss.AC003042	72070 72080 72090 72100 72110 72120 TCCTATGTGCCTTCTCAATCCCTGTTAATAAGAACACTGCCATTACAGCCATTAGAGT
ss.AC003042	72130 72140 72150 72160 72170 72180 CACCCAGGCTGGAAATCTGAGTTAATTCCAACCTTCTCCCTGGGTCTTCCTATTGAGTAGA
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ss.AC003042	72250 72260 72270 72280 72290 72300 GCATGGTTTAAGTTGCCTATGCTATATATATATATATACACATATATATACATATATATA
ss.AC003042	72310 72320 72330 72340 72350 72360 CATATACATATATACATATACACACACACACACACACACACACACACACATATA
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ss.AC003042	72430 72440 72450 72460 72470 72480 TGCCCAGGCTGGAGTGCAGTGGCGCCATCGAGGCTCACTGTAACCTCTGCCTCCTGGGTT
ss.AC003042	72490 72500 72510 72520 72530 72540 CAAGCGATTCTCCTGCCTCAGTCTCCCGAGTCGCTGGGATTACAGGCGCCACCACTACA
ss.AC003042	72550 72560 72570 72580 72590 72600 CCCAGCAAATTTTTTGTATTTTTTAGTAGAGACAGGGTTTCGCCAAGTTGGCCAGGCTGG
ss.AC003042	72610 72620 72630 72640 72650 72660 TCTTGAACCTCTTGACCTCAGGTGATCTGCCCCGCTCGGCCTCCCAAAGTGATGAGATTAC
ss.AC003042	72670 72680 72690 72700 72710 72720 AGGCTTGAGCTACCGCACCCAGCCCACTTTTTTTTTTTTTTAAAGCTTCTTAAGTACTT
ss.AC003042	72730 72740 72750 72760 72770 72780 TCCTGTTTCCACTCTTCCTAGCATTGACGCATCTCTTATACCAAATAATTTTCTAGCA
ss.AC003042	72790 72800 72810 72820 72830 72840 CAAATCTGATTATCTGTGTCTCAGCTTAAAAACCTTTCAGCTGGCCAGGCGTGGTTGCTC
ss.AC003042	72850 72860 72870 72880 72890 72900 ACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCAGGTAACCTGAGGTTGGGAGT
ss.AC003042	72910 72920 72930 72940 72950 72960 TCGAGACCAGCCTGACCAACATGGAGAAACCTGGTCTCTAATAAAATACAAAAATTAGCC
	72970 72980 72990 73000 73010 73020

ss.AC003042	GGGCGTGGTGGCGCATGCCTGTAATCCCAGCTACTCCGGAGGCAGAGGCAGGAGAATCAC
ss.AC003042	73030 73040 73050 73060 73070 73080 TTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGATCACACCACTGCACTCCAGCCTGG
ss.AC003042	73090 73100 73110 73120 73130 73140 GCAACAAGAGCAAACTCTGTCTCAAAAAAACAACAAACAAACAACTTTTCAGT
ss.AC003042	73150 73160 73170 73180 73190 73200 TGTCTCTTATTATTAATACTTCTGATTTACACTCTTCTTCGTGTTTTTTTTTTTAAAGA
ss.AC003042	73210 73220 73230 73240 73250 73260 TGGAGTTTCACTCTGTCAACCAAGCTGGAGTGCGGTGGGGCGATCTTGGCTCACTGCAAC
ss.AC003042	73270 73280 73290 73300 73310 73320 CCCCGCCCCCAGGTTCAAGCAATTCTCCTGCCTCAGACTCCTGAGTAGGTGGGATTACA
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ss.AC003042	73390 73400 73410 73420 73430 73440 GTTGGCCAGGCTGGTCTTGAACCTCTGACCTCAAAGTGATCCCCCACCTCAGCCTCCA
ss.AC003042	73450 73460 73470 73480 73490 73500 AAGTGTTGGGATTACAAGCATCAGCCACCACGCCCGCCTAGACTTCTTACTATAGTATT
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ss.AC003042	73750 73760 73770 73780 73790 73800 TACACCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATTGCTTGAACCCGGGAG
ss.AC003042	73810 73820 73830 73840 73850 73860 GCAGAGGTTGCAGTGAGCCAAGATCGCACCACCTGCACTCCAGCCTGCATAAGAAGAGCGA
ss.AC003042	73870 73880 73890 73900 73910 73920 AACTCCATCTCAAAAAAAAAAAAAAAAAAATATATATATATATATATATATATATATA
ss.AC003042	73930 73940 73950 73960 73970 73980 TATATATGTTACATTAGAGGCTCTAAGCCCACTTGGTAAACAGAGGCAACAATGCTGACA
ss.AC003042	73990 74000 74010 74020 74030 74040 AATAATGTTAAATTATGTTATTTCACTAAAGTTTTAAATATGGGCAAAAATATACAAAA
ss.AC003042	74050 74060 74070 74080 74090 74100 TTAACACAAAATGGATTAAAACTAAATGTTAACATCTGAAAACCATAAAACTAGAAGAA
	74110 74120 74130 74140 74150 74160

ss.AC003042	AACATAGGGGAAACTCTTCATGACACTGGACTAAGTGATGATTTCTGGCTATGACACCA
	74170 74180 74190 74200 74210 74220
ss.AC003042	AAAGCACACATGCACAACAAAAACAAAATAGATGCTTCTCTGAGAAAACACCAAATGGC
	74230 74240 74250 74260 74270 74280
ss.AC003042	AGATGATGCTGGTGGCAGCCGGTGGTGGGGATCGCCTGGGATGGGGAAATGCAGTGGCTT
	74290 74300 74310 74320 74330 74340
ss.AC003042	CCGTGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGCTGGGGCTGAGGCCGCGGCTGAGG
	74350 74360 74370 74380 74390 74400
ss.AC003042	CCGCAGAGCTCATGGAGGCAAGGCCGAGGATAAAGAGTGGATGCCTATCACCAAGCTGGG
	74410 74420 74430 74440 74450 74460
ss.AC003042	CCGCCTGGTCAAGCACATGAAGATCAAGTCCCTGGAGGAGATGTATGTCTTCTCCCTGCC
	74470 74480 74490 74500 74510 74520
ss.AC003042	CATGAAGGAATCTGAGATCACTAACTTTTTCTGGGGCCTCTCTCAAGGACGAGGTTTT
	74530 74540 74550 74560 74570 74580
ss.AC003042	GAAGATTATGCCAGTGCAGAAGCAGACCCGTGCCGGCCAGCGCACCAGGTTCAAGATGTT
	74590 74600 74610 74620 74630 74640
ss.AC003042	TGTTGCCATCGTGGACTACAATGGCCACATCGGTCTGGGTGTTAAGTGCTCCAAGGAGGT
	74650 74660 74670 74680 74690 74700
ss.AC003042	GGCCACTGCCATCCACGGGGCCATCATCCTGGCCAAGCTCTCTATTGTCCCTGTGCACAG
	74710 74720 74730 74740 74750 74760
ss.AC003042	AGGCTACTGGGGGAACAAGATCAGCAAGCCCCACACCATCCCTTGCAAGCCGACAGGCCA
	74770 74780 74790 74800 74810 74820
ss.AC003042	CCACGGCTCTGTGCTGGTGC GCCTCATCCCTACGCCCAGAGGCACTGGCATCGTCTCAGT
	74830 74840 74850 74860 74870 74880
ss.AC003042	GCCTGTACCCAAGAAGCTGCTTATGATGGCTGGTATTGATGACTGCTACACCTTAGCCAG
	74890 74900 74910 74920 74930 74940
ss.AC003042	GGGCTACACTGCCGCCCTGGGTAACATACCAAGGACACCTTTGATGCCATCTCTAAGAC
	74950 74960 74970 74980 74990 75000
ss.AC003042	CTACAGCTACCTGACCCCCGACCTCTGGAAGGAGACTGTATTCATCAAGTCTTCCTGTCA
	75010 75020 75030 75040 75050 75060
ss.AC003042	GGAATTCAGTACCATCTCGTCAAGACCCACACCAGAGTCTCCATGCAGAGGACCCAGGC
	75070 75080 75090 75100 75110 75120
ss.AC003042	TCCAGCTGTGGCTACAACACAGGTTTTTATACAAGAAAAATAAAGTGAATTAAGCCTGA
	75130 75140 75150 75160 75170 75180
ss.AC003042	AAAAAAAAAAAAAGACTACAGTCGTGTCACTTAACAATGGGACACATTCTGAGAAATGCA
	75190 75200 75210 75220 75230 75240
ss.AC003042	TTGTTAGCTATTTTGTGTGCTGTGCGAACATCAGAGTGTACTTACACAAACCTAGGTAGTA
	75250 75260 75270 75280 75290 75300

ss.AC003042	TACATATTTTTATTTATATTTTTTTTACATGGAAAACCAAATGTCCCAGCACCATCACTG
ss.AC003042	75310 75320 75330 75340 75350 75360 AATATTAATCATTTCTCTACTTGATCTGCAACGCAGTATGCTCCATTATAATCTTACGG
ss.AC003042	75370 75380 75390 75400 75410 75420 GCCCCTGTGCATATATGTGGTCTATCACTGACCAAATGTCATCACATAGCACATGACTA
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ss.AC003042	75490 75500 75510 75520 75530 75540 AAAGAATGGGAAAAAATATTTGCAAACCATATATTGAATAAGGGGTTAATAGCCAGAATA
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ss.AC003042	75730 75740 75750 75760 75770 75780 ATACAAATGGCCAGCAAACATATGAAAAGATGCTCAACATCACTAATCATCAGGAAAATG
ss.AC003042	75790 75800 75810 75820 75830 75840 CACATCAAAAACACAATGAGATATCACCTTAAACCAACTAGAATGACCACTATCAAAACA
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ss.AC003042	76090 76100 76110 76120 76130 76140 GCGAAATGTGAGAGCAACCTTCAATGTCCATCAATGTATGAATGGACAAAGAAATGTGAA
ss.AC003042	76150 76160 76170 76180 76190 76200 TAGCCAGGTGCGGTAATCCCAGCACTTTGGGAGACCGAGGCGAATGGATCACTTGAGGTC
ss.AC003042	76210 76220 76230 76240 76250 76260 TGGAGTTCAAGACCAGCCTGACCAACAAGGTGAAACCTGTCTCTACTAAAAACACAAAA
ss.AC003042	76270 76280 76290 76300 76310 76320 ATTAGCCAGGTGTGGTGGTGTGTGCCTGTAATCCCAGCTACTCAGGAGGCTGAGGCAGGA
ss.AC003042	76330 76340 76350 76360 76370 76380 GAATCACTTGAACCTCGGGAGGCGGAGGTTGCAGTGAACCGAGATCAAGCCACTGCACCCC
	76390 76400 76410 76420 76430 76440

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ss.AC003042	76510 76520 76530 76540 76550 76560 CTTTTAGAGGGGAATCCTGTCTATGCTACAACATAGATGAATCTTAGACATTATCTAAG
ss.AC003042	76570 76580 76590 76600 76610 76620 TATTGTCTTAGATAATGGCTAAGTAAATAAGCCAATCACAAAATTCAAGTGCTACATT
ss.AC003042	76630 76640 76650 76660 76670 76680 ATCCCATTTATATGAGCTATCTAAAATAATTAAACTCAGAAACAGAAAGAAGAATTGTGG
ss.AC003042	76690 76700 76710 76720 76730 76740 TTGCTAGGGGGTGAGGGGAGAAAAAGGTGTTGTTCAATGCGTATAGTTTCAGTTGAGAT
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ss.AC003042	76870 76880 76890 76900 76910 76920 ACTCTGTTGCCCAGGCTGGAGTGCAGTGGCATACTCTTGTCTCACTGTAGCCTCAACCTC
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ss.AC003042	77110 77120 77130 77140 77150 77160 CTGAACGTGTGAGACACTGTGCTTAGCCTTATTTTGTGTTCTTTTAAATATACACATACG
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ss.AC003042	77230 77240 77250 77260 77270 77280 AATACTTCCACATTTTCAGGTTATAAACAGCAAGTTCACATTTTCAGGTAATTAAATGGT
ss.AC003042	77290 77300 77310 77320 77330 77340 CAAATATCAAAGAGAACAATAAAACTTGAAATATTTTCCCCCTATTTTACTGCTTTA
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ss.AC003042	77410 77420 77430 77440 77450 77460 AGTTAAAAATAGGATATAAAAGCCGTAAAAGCTTTTTTCCCATTGCAAAAGCAGCATTG
ss.AC003042	77470 77480 77490 77500 77510 77520 CATATGACTTTTTTAAACCTTTTTTTTTTCGAGACAGAGTCTCACTCTGTCACCCAGGCT
	77530 77540 77550 77560 77570 77580

ss.AC003042	GAAGTGCAGTGGCATGATCATGGCTCACTGCAGCCTTCAACCTTCCTGGGCTCAAGTGAT
ss.AC003042	77590 77600 77610 77620 77630 77640 CCTCCACCTCAGCCTCCCGAGTAGATGAACTGCAGGTGTGTCCTACGCCCAGCTAAT
ss.AC003042	77650 77660 77670 77680 77690 77700 TTTTTTATTTTGTGTTTTATATTTATTTATTTTATTTTACTATTATCTTTTTTTTGA
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ss.AC003042	77770 77780 77790 77800 77810 77820 AGTTCCGCCTCCTCGGTTACGCCATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTA
ss.AC003042	77830 77840 77850 77860 77870 77880 CAGGCGCCCGCCATCAAGCCCGGCTAAATTTTTTGTATTTTTTAGTAGAGATGGGGTTTC
ss.AC003042	77890 77900 77910 77920 77930 77940 ACAGTGTTAGCCAGGATAGTCTCAATCTCCTGACCTCATGATCCGCCC GCCTCGGCCTCC
ss.AC003042	77950 77960 77970 77980 77990 78000 CAAAGTGCTGGGATTACAGGCGTGAGCCATGGCACCCGGCCTGTTTTTTTTGTGAGATGG
ss.AC003042	78010 78020 78030 78040 78050 78060 AGTCTTGCTGTTGCCGAGGCTGGAGAGCAAATGGCGTAATCTTGGCTCACCGCAACCTCC
ss.AC003042	78070 78080 78090 78100 78110 78120 ACCTCTCAGGTAAAGTGATTCTCCTGCTTCAGCCTCCTGAGTAGCTGGGATTACAGGCAC
ss.AC003042	78130 78140 78150 78160 78170 78180 ACGCCACCAAGCCCGGCTAATTTTTGTATTTTTTAGTAGAGACGGGGTATCACCATGTTGG
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ss.AC003042	78250 78260 78270 78280 78290 78300 AGATTAGAGGAGTGAGCCACCACACTCAGCCTTTATAAATGGGCCTCCCTATGTTGCCCA
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ss.AC003042	78370 78380 78390 78400 78410 78420 AATTATAGGCTTGAGCCACAATGCCAGCCTTAAAAAACCCCTTAAGGCAGAGGTTTCAGT
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ss.AC003042	78490 78500 78510 78520 78530 78540 GTGTAGTATCTGCCGATGTTCTACCGTAATACTTTTCTTTTGAGACAGAGTCTCACTCTG
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	78670 78680 78690 78700 78710 78720

ss.AC003042	GCCTGGCTAATTTATGTATTTTCAGTAGAGAGGGGTTTCACCATGTTGGCCAGGCTGGTC
	78730 78740 78750 78760 78770 78780
ss.AC003042	TCAAACCTCCTGGCCTCATGTGATCTGCCCATTTACGCTCCCAAAGTGCTAGGATTACAG
	78790 78800 78810 78820 78830 78840
ss.AC003042	GCATGAGCCACCATGCCCGGCTCTACCGTAATTCTTTTTTTGTTGTTGTTTTTTGGGA
	78850 78860 78870 78880 78890 78900
ss.AC003042	ACGAAGTTTCACTCTTGTTGCCAGGCTGGAGCGCAATGGCGCATCTCAGTTTACTGCA
	78910 78920 78930 78940 78950 78960
ss.AC003042	ACCTCTGCCTCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGCTCCTGAGTAGTTGGGA
	78970 78980 78990 79000 79010 79020
ss.AC003042	TTATAGGCACCCACCACCGCCAGCTAATTTTTGTATATTTAGTAGAGATGGGGTTTC
	79030 79040 79050 79060 79070 79080
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	79090 79100 79110 79120 79130 79140
ss.AC003042	CCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCACCCAGCTGCTAATTTTATTTTAAT
	79150 79160 79170 79180 79190 79200
ss.AC003042	TTTTATTATTTTTGAGATGGCGTTTCACTCTGTTGCTCAAGCTGGAGTGCAGTGGTACAA
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ss.AC003042	TCACGGCCACTGTGATCATGGTGCACCTTCAACCTCCTGGGCTCAAGTGATACTCTCAC
	79270 79280 79290 79300 79310 79320
ss.AC003042	TCACCCTCCCCAGTAGCTAGGACTACAGTTTGTGCCACCATGGCAGCTAATTTTCTGC
	79330 79340 79350 79360 79370 79380
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	79390 79400 79410 79420 79430 79440
ss.AC003042	AACCATCTACCTGACTTGGCCTCCCAAAGTGCTGGAACCTACAGTTGTGAGCCACCATGCC
	79450 79460 79470 79480 79490 79500
ss.AC003042	CAGCCTATGTTTGTTTTAAAGAAGACAAAATTGAGGCACAGAAAGTCAACTAATTGTA
	79510 79520 79530 79540 79550 79560
ss.AC003042	CAGTTACAATTAGTAGAATCCAGATGCAATACAATCTCCCTAAATTCATCACTCACTGCC
	79570 79580 79590 79600 79610 79620
ss.AC003042	TTAATTATTATTACTCTCAACCATACTTTCTCACAACCGTTAAGATATCTGTAAAATGGA
	79630 79640 79650 79660 79670 79680
ss.AC003042	CTAAAATCCATCTAAAATGTTAAACACTAACCTAAACATAGGAAAATCTACAAAACC
	79690 79700 79710 79720 79730 79740
ss.AC003042	ATTATAAGAACTCCAAAACATGTGCTCTAATAACTTGTCAATTTATCACCTGCAAAAAC
	79750 79760 79770 79780 79790 79800
ss.AC003042	ATCTTTTGGGAGGATCAATTCATATTTAAAGAGGAAGGATATATGTTTTGTGTCTGTATA
	79810 79820 79830 79840 79850 79860

ss.AC003042	GTCCCTGTAAAACTCCAAGTAAGTGACACATTCTCTACTCTCTTGGGCATAATCCACCAA
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ss.AC003042	80530 80540 80550 80560 80570 80580 AGCACTTCGGGAGGCTGAGGAGAGCGGATCACAAGTCAGGAGACTGAGACCATCCTGGCA
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ss.AC003042	80650 80660 80670 80680 80690 80700 GCCTGTAATCCCAGCTACTTGGGAGGGTGAGGCAGGAGAATCTCTTGAACCAGGGAGTCA
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ss.AC003042	80830 80840 80850 80860 80870 80880 TGAAGTTACTTTTATAGTAACAAAACACATGAATATCAACTCTCTTTTGGGGTCTTGATA
ss.AC003042	80890 80900 80910 80920 80930 80940 ATGACAGAAGAAATACTTCAAATATTAAGTAAAAAGCTACTAATTTAATTTTGAAAATGC
	80950 80960 80970 80980 80990 81000

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ss.AC003042	81010 81020 81030 81040 81050 81060 TGGATTACCTGAGGTCAGGAGTTTCGAGACCAGCCTGAACAACATGGCGAAGCCCCGTCTC
ss.AC003042	81070 81080 81090 81100 81110 81120 TACTAAAAATACAAAAATTAGCCGGGCGTGGTGGCATGCGCCTGTAGTCTCAGCTACTCA
ss.AC003042	81130 81140 81150 81160 81170 81180 GGAGGCTGAGGCAGGAGAACCGCTGGAACGCGGGAGGCGGAGGGAACAGTGATCCGAGGT
ss.AC003042	81190 81200 81210 81220 81230 81240 CTCGCTACTGCACTCCAGCCTGGGTGACAGAGTGCAACTCTGTCTCAAAAAGAAAAAAA
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ss.AC003042	81310 81320 81330 81340 81350 81360 CATAAAGCAACTGCTTTGGCCAAGCGCAGTGGCTCATGCCTGTAATCCTAGCACTTTGGG
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ss.AC003042	81430 81440 81450 81460 81470 81480 AACCCCATCTCTACTAGAAATACAAAAATTAGCTGGGTGTGGCGGCGTATGCCTGTAATC
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ss.AC003042	81670 81680 81690 81700 81710 81720 AAGGCTAGAATGCTATTATACAAAGGAGTTTCAGTGACAGGCCACTCTAGGTGACTGACAC
ss.AC003042	81730 81740 81750 81760 81770 81780 ATAAGGCACCTTCCACATTATACTGGAACAACCATCAGACTTACCTGTGTTTTTCGCAGAT
ss.AC003042	81790 81800 81810 81820 81830 81840 ATGTTTCTAGTGTCTTCTAAAAGACAACCTCGAGTCAATTAAACTACTTCATCCCTGCATT
ss.AC003042	81850 81860 81870 81880 81890 81900 CCTGCGACATTAGTTCCCATACATCCATCCAACAACCTCTGTAGAAAGAACAATATTAG
ss.AC003042	81910 81920 81930 81940 81950 81960 TGAAAAGGGAGAATACAGAAGGGTAAACCTTAAAAAACAAAAACAGATTAAAGTATT
ss.AC003042	81970 81980 81990 82000 82010 82020 GCTTGTTTTTACCTGGCTGTTCCCTGGAAACGTCCATAATGGAAAATGATCCTATACTTG
ss.AC003042	82030 82040 82050 82060 82070 82080 CCGTCCTTCCTGTGGCCTTCACTATTTCTCATCTGTACTTAACTTCTCTGAACTGACACT
	82090 82100 82110 82120 82130 82140

ss.AC003042	GCTACTGCTCCCTTCACCGTAGTATAGTACAAAGCTTAGTGACACTGAGATAATCTGAAG
ss.AC003042	82150 82160 82170 82180 82190 82200 AAATAATTTCTATAGTCTAAATTAAAATCATGAACACTTTAATGATTAAGATATTAGAAC
ss.AC003042	82210 82220 82230 82240 82250 82260 ATGTTTACAAATTATATGATTACATACTCACTTTATATTAATATAACGTTTCATTTAAATG
ss.AC003042	82270 82280 82290 82300 82310 82320 TGTGCTCATATCTTTATATAAAACTTCTGCTTGACTATCAAGTTTATCTGATACAATTT
ss.AC003042	82330 82340 82350 82360 82370 82380 AACAACATCTGTAGTTATCAAGAGAGCAACTGGTTAATAAACTAAGTATTCTATGAGCAA
ss.AC003042	82390 82400 82410 82420 82430 82440 ATATAGTTGGAATGTTCTAAAGTCAAATGACCGAAAAATTATCAAGTATTTTCCCTTT
ss.AC003042	82450 82460 82470 82480 82490 82500 TAAACACAGACCAATCTTCCACAAATTGAAAATTCTAAGAAGTTTGTATCTACTTAATGA
ss.AC003042	82510 82520 82530 82540 82550 82560 GATCATCATCAAGTAATTTTTTTTTTACTTTTATTTTGTAGAGACAAGGTCTCTACTATG
ss.AC003042	82570 82580 82590 82600 82610 82620 TTGCCCAGCCTGGCCTCAAACCCCTGACCTCAAGCCATTCTCCACCTCAGCCTCCCAA
ss.AC003042	82630 82640 82650 82660 82670 82680 GCACTGGGATTACAGGTGTGAGCCACCATGCTCAGCTCAATTTTTTTTTTGTAACTACTC
ss.AC003042	82690 82700 82710 82720 82730 82740 CTTTTTAAAGCTAAACCATGGTAACAAACTATCATCTACCTTCACATGTATAAGTAGCT
ss.AC003042	82750 82760 82770 82780 82790 82800 GGGAAGGTCATAGATTAATTACAGTGAATAAGTTTTACATTTACTAAAAGATAGTACACT
ss.AC003042	82810 82820 82830 82840 82850 82860 AAGACGAACACTTTATACAGCCTAAATTAATAAGAACTATGTGGTAATTTTTTTTTTTTT
ss.AC003042	82870 82880 82890 82900 82910 82920 GAGACAGATTCTCGCTCTGTCACTCAGGCTGGAATGCAGTGGCGTGATCTTGGCTCAGTG
ss.AC003042	82930 82940 82950 82960 82970 82980 CAACCCACCCCTGCAGGGGCTCAAGTGATCCTCCTACCTCAGCCTCCCGAATAGCTAGG
ss.AC003042	82990 83000 83010 83020 83030 83040 ACCATAGGCGTGTAACCAACACACCAGGTTATTTTTATTTTTTATTTTTTGTATTTTTTA
ss.AC003042	83050 83060 83070 83080 83090 83100 AGTAGAGACAGCAGGGTCTTGTCATGTTGCCAGGCTGATCTCCGACTCCTCAGCTCAAG
ss.AC003042	83110 83120 83130 83140 83150 83160 CAATCCACCCACCTCAGCCTCCCAAAGGGCTGGGATTACAGGCGTGAGCCACCAAGCCCA
ss.AC003042	83170 83180 83190 83200 83210 83220 GCCCTATACAATTTTTTAACAACTTACTAAAACTTCCCACTCTCCCTCCCCAACAGGG
	83230 83240 83250 83260 83270 83280

ss.AC003042	TTCAACTTCAGTATGAAAATTGCCACACATTTTGCTTTGTTGCAGCACATTTATCTTGGA
ss.AC003042	83290 83300 83310 83320 83330 83340 CCTGCATTCCAAGGGAAATGTGGGTTTACACTCCATTCAATCACAGCCTTCTTGATTTTT
ss.AC003042	83350 83360 83370 83380 83390 83400 CATGATTCTGAACAACTGGCTCCTGTCTGTTCTTCTGCAGGTCTCAGTACAGTCCAAGGA
ss.AC003042	83410 83420 83430 83440 83450 83460 ATTCATTACACCTTGGACGCCAGAGACGGAAAAACCTCTGAACTTTTAACTTACTCTATG
ss.AC003042	83470 83480 83490 83500 83510 83520 TAGCTAAATGGGTATTTCTCAACCCTCTGCCTAAAATGTAAGTTATCCACACAATTACAGC
ss.AC003042	83530 83540 83550 83560 83570 83580 TCTGTACTCCCTCTCACAAGGGCTCAGGCCAAGGTTTAGCTCCCCTTATTTGTGACAACA
ss.AC003042	83590 83600 83610 83620 83630 83640 AAAACATCATCTGTTCCACTTTCCATGCTACATCCTTCTATTCTCAACTCTGATATTTCC
ss.AC003042	83650 83660 83670 83680 83690 83700 TTTTTGAGACAGAGTCTCACTCTGTGCGCCAAGCTGGAGTGCAGTGGTGTGATCTCGGCT
ss.AC003042	83710 83720 83730 83740 83750 83760 CACTGCAACCTCCGCCTCCCAGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCT
ss.AC003042	83770 83780 83790 83800 83810 83820 GGGACTACAGGCGTGTGCTACACACCTGGCTAATTTTTGTATTTTTAGTAGAGACGGGG
ss.AC003042	83830 83840 83850 83860 83870 83880 TTTCGCCATATTGGCCAGGCTGGTCGCGAACTCCTGACCTCGTGATCTGCCTGCATCGGC
ss.AC003042	83890 83900 83910 83920 83930 83940 CTCCCAAAGTGCTGGGATTACAGTGTGAGCCACCCCGCCAGCCCCTTTTATTA ACTAT
ss.AC003042	83950 83960 83970 83980 83990 84000 ACTTGATCAGTATAATGCATAATTTCCCAGAACTGAAAACTCTCAAACCTCAAGCTCTCA
ss.AC003042	84010 84020 84030 84040 84050 84060 TAATTGAGGGAAAGGTTTATAAAGAGAAATCAGCTAAAGAATGATTATTATATCATTAGA
ss.AC003042	84070 84080 84090 84100 84110 84120 ATGTGAAGGCATTTTTTTTTTAAAAAAAAGCTCTATAAAAAAATCTGTATCTCAAATCA
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ss.AC003042	84250 84260 84270 84280 84290 84300 AATCCATGACAACCTTACATTGCATTCACTTTTCAATCATTGCAACCTGGATTCTGCTTC
ss.AC003042	84310 84320 84330 84340 84350 84360 CACTCAATCACTAGCTCAGCTCTTCAAGATCACCAATTATCTCATTGTTACTAAATCCAA
	84370 84380 84390 84400 84410 84420

ss.AC003042	TGTCCACTTTTGGGTCCTTGATAACTTGGCCGCATTTAATATAGTTGATCAGACTTCCTT
ss.AC003042	84430 84440 84450 84460 84470 84480 GGAACGCTTTTACACCTTGGCTTCCTTCTACCTATCTGGCTACTCTTTCTCAGGTTTCTT
ss.AC003042	84490 84500 84510 84520 84530 84540 TACTAATTTCTTTTCTACCATTAAATTCCTCAGAATTCTTTTACTCTCTTTCCCTTTAGG
ss.AC003042	84550 84560 84570 84580 84590 84600 TGATCTTACATAACATTCTCTAAGATAAACTACAGGCCTACAACCTCCAGCCTAGATCTTT
ss.AC003042	84610 84620 84630 84640 84650 84660 CTTCCAGATCTCAAACCTTACTCCCAGACAGACAATAACCTGGGTTTACTTGCATAGATGA
ss.AC003042	84670 84680 84690 84700 84710 84720 GAGAATACTCTCAGAAAGGCTGACCTAGATTTCTATTTATTAGGCTAAAACCTAATCAAC
ss.AC003042	84730 84740 84750 84760 84770 84780 TGTATTATACTTTTCTCTGGAAATAGACTAAACAAATTAAAAAGCTATGGGGGGTGGGGA
ss.AC003042	84790 84800 84810 84820 84830 84840 TGTAGCAGCAGGAGGGGGAGTGGAAATACATAAAATGGAGAATCATAGTAGCATTTAATA
ss.AC003042	84850 84860 84870 84880 84890 84900 GTGGTGACCATCCAAGGGAGAGGGAGCCTTGGCTAAGCATACTGTACTGCTTAGCCTGCT
ss.AC003042	84910 84920 84930 84940 84950 84960 ATTCTATGTGGCCTGTGGGAATAACTGAAGCTACCTTAATCAAGAGACAGACACCACTTA
ss.AC003042	84970 84980 84990 85000 85010 85020 AGATCAATTAAGTCCATTACACTGATTCCATACTCAGCAAACAGCCTTCTAAAACATAT
ss.AC003042	85030 85040 85050 85060 85070 85080 GACTTCCCATGTAGTGGAAGTGTAGCTAGAAGGGGATGTAAAATCTGTGGAGGTTTGT
ss.AC003042	85090 85100 85110 85120 85130 85140 TGTTTCTTAAGCTGAAAGATAGGAAAACAGAGCTGAATGTAAATTTAACAAAAGTAGGTA
ss.AC003042	85150 85160 85170 85180 85190 85200 ACTGAATAAGCAAAGTGATTGAAAACAAAGAAAATGGAGTGCAGAGCAAGAGTGGAAGGA
ss.AC003042	85210 85220 85230 85240 85250 85260 TTGGTCTTTGAAGGAAGGCAGCAATGAACACAGATGCATAAAATGCTGGGCTACTTGCTT
ss.AC003042	85270 85280 85290 85300 85310 85320 CTCAGTTCATCAACAAAGAATATGCTTAACAGAAAAAAGCACCAGAAGGCAAGCTCTTT
ss.AC003042	85330 85340 85350 85360 85370 85380 ACTGTATCATACCACTTTAGGCCTTCAGCCAACAGGTCATCTCTAATGTGAAAAATTAGC
ss.AC003042	85390 85400 85410 85420 85430 85440 CTGTAATCTGCATTTAGAGTCAGAAATTTCTCTGAAGCTACTGACAAATCTGAGAAGGAAG
ss.AC003042	85450 85460 85470 85480 85490 85500 AATGAGCTGATGAAAAAATAAAAAATAAAAAATTTTAAAAAGATACTGACAAATTGGGCC
	85510 85520 85530 85540 85550 85560

ss.AC003042	AGGCGCCGTGGCTCACGCCTGTTAATCCCAACACTTTGGGAGGCCAAGGCGGGTTGATCA
ss.AC003042	85570 85580 85590 85600 85610 85620 CCTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACCTGGTGAAACCCTGTGTCTACTAAA
ss.AC003042	85630 85640 85650 85660 85670 85680 AATACAAAATTAGCCGGGCATGGTAGCAGGTGCCTGTAATCCCAGCTACTTGGGAGGCT
ss.AC003042	85690 85700 85710 85720 85730 85740 GAGGCAGGAGAATCACTTGAACCCAGGCGGCAGAGGTTGCAGTGAGCCGAGATCGCGCCA
ss.AC003042	85750 85760 85770 85780 85790 85800 CTGCACTCTAGCCCGGGTGACAGGGGAAATTCCATCTCAAAAAAAAAAAAAAGAATTTGAA
ss.AC003042	85810 85820 85830 85840 85850 85860 AGAAAGAAAAAAAAAAGATACTGACAAATCAAGCAGCAAAATAACAACCTATCCTTAAGAA
ss.AC003042	85870 85880 85890 85900 85910 85920 AACTTCTTTTCTTCAGGCTACAAGAACATAATGTGTGGTTCTTGTGTTGGATCCTGATTCA
ss.AC003042	85930 85940 85950 85960 85970 85980 TACAAACCAACATTCAAAAAAAAAAAAAAACCAGAAACAGGTAAAATCTAAGTATGAAC
ss.AC003042	85990 86000 86010 86020 86030 86040 TGGGTATTTCGATTGTTACACTTAATTTTGTAGGTGTTATGATGGCAATGTGTGAAAAAA
ss.AC003042	86050 86060 86070 86080 86090 86100 AATGTCCATATATTTAGAGATGCATGTGGAAGGATGCAATAGAGTAACACGAAGCCTGGG
ss.AC003042	86110 86120 86130 86140 86150 86160 ACTTGCTTTTAAAATACAAAGAAAAAGGTGGATAAATGAAGCAAGTGTGGCAACTCTTGAT
ss.AC003042	86170 86180 86190 86200 86210 86220 TACTACTAAATCTTGGTAAAAGTGCATGGGAGGTTCAATCATTGTATTTTTTTACTTTTCT
ss.AC003042	86230 86240 86250 86260 86270 86280 ATGTTTGACAATTTTACTAATAAAATTTATTTTATTTATTTATTTATTTATTTTCGAGACA
ss.AC003042	86290 86300 86310 86320 86330 86340 AAGTCTCACTCTTGTCGCCCAGGCTGGAGTGCAATGGTGCATCTTGGCTCAATGCAACC
ss.AC003042	86350 86360 86370 86380 86390 86400 TCTGCCTCCTGGATTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTAAGATTACAA
ss.AC003042	86410 86420 86430 86440 86450 86460 GCACCTGCCACCACGCCTGGCTAATTTTTGTATTTTTTAGTAGAGACAGGGTTTCACCATG
ss.AC003042	86470 86480 86490 86500 86510 86520 TTGGCCAGGCCGGTCTCGAACCCCGACCTCAGAGAATCCACCCAACCTGGCCTCCCAA
ss.AC003042	86530 86540 86550 86560 86570 86580 GTGCTGGGATTACAGGCGTGAGCCACCACGCCAGCCTTTTTTTTTTTTTTTTTTTTTT
ss.AC003042	86590 86600 86610 86620 86630 86640 TTTTTTGAGACAGAGTCTCGCTCTGTCGCCCAGGCGACACGATCTCAGCTCACTGCAACC
	86650 86660 86670 86680 86690 86700

ss.AC003042	TCCACCTCTTGGGTTCAAGCAATTCTCCTGCCTCAGCCTCCTAAGTAGCTGGGATCACAG
ss.AC003042	86710 86720 86730 86740 86750 86760 ATGTGTGCCACCATGCCTGGCTAATTTTTATATTTTAGTAGAGATGAGGTTTCCCCATG
ss.AC003042	86770 86780 86790 86800 86810 86820 TTGGTCAGGCTGGTCTCGAACTCCTGACCTTGTGATCTGCTCGTCTCGGCCTCCAAAAGT
ss.AC003042	86830 86840 86850 86860 86870 86880 GCTGGGATTACAGGCATGAGCCACTGCACCCGGCCGATAAAATGTTTTAAATATTTTTTG
ss.AC003042	86890 86900 86910 86920 86930 86940 TTGCTCGGTATAGGGGAAAAAACTTAATAGATTATTAACATAACCACTGCCTGGTCATCC
ss.AC003042	86950 86960 86970 86980 86990 87000 AAGTCTTTGTGTGTCAGGGAGGAAAATGTCTATACAATAATGGTGTAACCTCGGAAGTTCAGG
ss.AC003042	87010 87020 87030 87040 87050 87060 TCAAAAAAAAAAAAAAATCAAAAAAGGTGACAATGACACAAATGAGATATTTAAAAATT
ss.AC003042	87070 87080 87090 87100 87110 87120 AACTTTTCAGAGGCCAGGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGACCA
ss.AC003042	87130 87140 87150 87160 87170 87180 AGTCAGGCAGATCACTTGAGGCCAGGAGTTTGAGATCAGCCTGGGCAACATGGCGAAACC
ss.AC003042	87190 87200 87210 87220 87230 87240 CCGTCTCTATTAAAAATCCAAAAAATTAGCCAGGAGTGGTGGCGAACACCTGTAATCCC
ss.AC003042	87250 87260 87270 87280 87290 87300 AGCTACTCAGGAGGCTGAGGCACAAGAATTGCTTGAACCCAAGAGGCAGAGGTTGCATGA
ss.AC003042	87310 87320 87330 87340 87350 87360 GCTGAGATCGTACCACTGCACTCCAGCCTGAGTGACAGAGCAAGACTGTGTCTCAAAAAA
ss.AC003042	87370 87380 87390 87400 87410 87420 ATAATTAAAAGATAAAATTAATAAAGAAGTATAGTTTTTTAATATCCCATTCTCTCCAAA
ss.AC003042	87430 87440 87450 87460 87470 87480 ACTAAAGTCACGTCTTAGAAAGTCCCTTCACACTCCATGGCTTCGCCTCACTATCCCCAC
ss.AC003042	87490 87500 87510 87520 87530 87540 CCCCAGGCAATTTTGTAGGGGACAACATGGCACTGTGCTGGGAGAAAGTGAAAAAGCAG
ss.AC003042	87550 87560 87570 87580 87590 87600 CCTTGGACACTATAGCACTTAATCAAGAAGAAAACACAAATTATTATCAGGCAATATTT
ss.AC003042	87610 87620 87630 87640 87650 87660 GCTTAAAAAATAAAATAGGCCGGGCGCGGTGGCTCACGCCTGTAATCTCAGCACTTTGGG
ss.AC003042	87670 87680 87690 87700 87710 87720 AGGCCGAGGTGGGCGGATCATGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGA
ss.AC003042	87730 87740 87750 87760 87770 87780 AACCCTGTCTCTACCAAAAATACAAAAAATTAGCCGGGCTTGGTGGCACGCACCTGTAGT
	87790 87800 87810 87820 87830 87840

ss.AC003042	CCCAACTACTCGGGAGGCTGGGGCAGGAGAACAGCTTGAACCCAGGAGGCAGAGGTTGCA
ss.AC003042	87850 87860 87870 87880 87890 87900 GTGAGCCGAGATGACGCCACTGCACTCCAGCCTGGGCGACAGAGGAGACTCCATCTCAAA
ss.AC003042	87910 87920 87930 87940 87950 87960 AAATAATAATAAATATAGAAACTACAAATTAGTTACATAAATACATATTGTCATAATAT
ss.AC003042	87970 87980 87990 88000 88010 88020 CGTCATAACTACTTTTTTTAAACCTTGGTAAATTACAGCTAGAGACAAGAAAGATAAAT
ss.AC003042	88030 88040 88050 88060 88070 88080 AATTTATACATTATGACTATTCTGTAGATCAAATAATGATTACCACTACTTTGAAAACGT
ss.AC003042	88090 88100 88110 88120 88130 88140 TCATATTAGCTGCATACATTTCCATAAAGACTTCAACCGGCCGAGTGTGGTGCCTCACAC
ss.AC003042	88150 88160 88170 88180 88190 88200 CTGTAATCCCAGCACTTTGGAGGCTGAGGTGGGCGATCACCTGAGGTCAGGAGTCCGAGA
ss.AC003042	88210 88220 88230 88240 88250 88260 CCAGCCTGGCCAATAGGGTGAAACCCCATATCTACTAAAAATACAAAATTAGCCAGGTG
ss.AC003042	88270 88280 88290 88300 88310 88320 TGGTGGCACGCACCTGTAGTCCCAGCTACTCAGGAAGCTGAGGCAGGAGAATCATTTGAA
ss.AC003042	88330 88340 88350 88360 88370 88380 CCAGGGAGGTGGAGGTTGCAGTGAGCTGAGATTGTGCCACTGCACTCCAGCCTGGGAAAT
ss.AC003042	88390 88400 88410 88420 88430 88440 AAAGGGAGACTCCGTCTCAAAAAAAGAAAAAAGAACTTCAACCTCCCTCCTCTAAA
ss.AC003042	88450 88460 88470 88480 88490 88500 ACATATTTAACATAAAAAAATTTTTTTAAATCAGATCTACATTGAGACTTTATATATATC
ss.AC003042	88510 88520 88530 88540 88550 88560 AAGGCAAAATGGCCAACATAACAAGAGGATCTATTTATTTTGACCTATGTCATAGAGTAT
ss.AC003042	88570 88580 88590 88600 88610 88620 AACCAATTAATGAATTAAAGCAAACAGTGGGTTTATTTCTTTTACTAAATATGATCAAAT
ss.AC003042	88630 88640 88650 88660 88670 88680 ATATAATCTTAACAATGACAAAGCCTCTTGGTATTCAATTCTACTTACCCCAAAGGTTTT
ss.AC003042	88690 88700 88710 88720 88730 88740 GGCTTGTCGTATCTAAGGAGTGCAACTGACATCTCTTATTCTTCTTACTTTTTGGAATA
ss.AC003042	88750 88760 88770 88780 88790 88800 GCATCTATCATGTCAATTTAGTTTGGACCTAATTAAAAATAAAACATATTAAGGGTTTAAT
ss.AC003042	88810 88820 88830 88840 88850 88860 TCATTTTACTTTCAAATTTTAAATCTCTATTTACTGTCTTTTAGAGAGAAGTCTCAAAA
ss.AC003042	88870 88880 88890 88900 88910 88920 CAAAACACAAAAAACCACTTTTCTCTATCCCCACTGTATCTAGCAGTGTGCCTGGCACT
	88930 88940 88950 88960 88970 88980

ss.AC003042	CACGTTATTTCAACACTGACTGCTACCTGACTCTCAGCCATCTTCCCTTGCCCAGCCATT
ss.AC003042	88990 89000 89010 89020 89030 89040 ATGTAAATACACCAGTTGCAGAAGCACACACCTGTAGTCCCGGCTATTTGGGAGGCCGAG
ss.AC003042	89050 89060 89070 89080 89090 89100 GTGAAAGGATCACTTAAGCCCAAGGGTTTGAGACCAGCCAGGGCAACATAGTGAGATCCC
ss.AC003042	89110 89120 89130 89140 89150 89160 ATGTCTTTAAAAAATATATAAAAACCTCACAAAACATTATGTAAACACAATACATCCTTG
ss.AC003042	89170 89180 89190 89200 89210 89220 AAGAGGAGTCATCAACAGAACTTTTATGCAATATGGAATACACACTACTACTATCCGCA
ss.AC003042	89230 89240 89250 89260 89270 89280 CCTTCCATCCAACCAATGAGCAAAGTTTGCCAATTCTACCTTTTAAATATTATCTAGAAT
ss.AC003042	89290 89300 89310 89320 89330 89340 CAGGCCTGGTGCAGTAGCTCATGCCTATAATCCCAGCACTTTGGAAGGCTGAGGTAAGAG
ss.AC003042	89350 89360 89370 89380 89390 89400 GATCACTTGAGGCCAGGAGTTCAAAGCCAGCCTGGGTAACATAGCAAAATTTTCATCTCT
ss.AC003042	89410 89420 89430 89440 89450 89460 ACAGAAAATTTTAAATGAGGCCAGGCATGGTGGCTCACACCTGTAATCCCAGCACTTTG
ss.AC003042	89470 89480 89490 89500 89510 89520 GGAGACTGAGGCCAGGAGTTAAGAGACCAGCCTGGCCAACATGGAGAACTCTATTTCTG
ss.AC003042	89530 89540 89550 89560 89570 89580 CTAAAAAAATACAAAATTAGACAGGTGTGGTGGTGCACGCCTGTAATCCCAGCTTCTC
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ss.AC003042	89710 89720 89730 89740 89750 89760 TAAGATAGAATAAAAGCTAAATAAAAATTAACCAATCTAGAATCAGATCACTTCTTATCA
ss.AC003042	89770 89780 89790 89800 89810 89820 CCTCTACCATTATCATCCCTGTCCAACCCACCAATCTCTAGCTTAGTCAACTGCAATAGC
ss.AC003042	89830 89840 89850 89860 89870 89880 TGGCCTCCTAAATGGTCTCCTTGCTGCACCTTCTGCCCTTTACATTCCAGGCCTCACTCA
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ss.AC003042	89950 89960 89970 89980 89990 90000 ACTCCAAGGCTTATTTTCTCAAGCCCAGGCACAGTAAATATCAAAAGTCCCTACCACCAT
ss.AC003042	90010 90020 90030 90040 90050 90060 CTCTAAATAGGAAAGCCTCGGGTTTACTTTTCAGACCTCTTCTCTTTTCCCTATTTATAT
	90070 90080 90090 90100 90110 90120

ss.AC003042	TCACTAAATGAGACAAATTTACATCTCTAACCCAGACCTCTCTGAATTCTATTTGGATGT
ss.AC003042	90130 90140 90150 90160 90170 90180 CTAATCGCTATCTCAAACCTTAGCACACCCAAAGATGAGCTCTGTTACATTTCTCCTCAGT
ss.AC003042	90190 90200 90210 90220 90230 90240 CTCGTCCCTCTCGGTAAATGGTAACCATTTGCCCATTTCTTTTTTTTTTTTTTTTTTTTTTTT
ss.AC003042	90250 90260 90270 90280 90290 90300 TTTGAGACAGAGTCTCGCTCTGTTGCCACGCTGGACTGCAGTGGCGCAATCTTGCCCTCA
ss.AC003042	90310 90320 90330 90340 90350 90360 CTGCAACCTCCGCCTCCCGGGTTCAAGCGATTCCCGTCTCAGCCTCCTGAGTAGCTGGGA
ss.AC003042	90370 90380 90390 90400 90410 90420 TTACAGGTGCCTGCCACCACGCCCCGGCTAATTTTTTATTTTTTAGTAGAAATGGGGTTTCA
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ss.AC003042	90490 90500 90510 90520 90530 90540 CCAAAGTGCTGGGATTATAGGTGTGAGCAACCACGCAAGGCCTGTTGTCCATTCTTTACA
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ss.AC003042	90610 90620 90630 90640 90650 90660 CACTGGCTCATTCCTCAAAATATATCCAGGATCCTTTATAACCATTTTTTCACTACCTCCA
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ss.AC003042	90850 90860 90870 90880 90890 90900 CAGATCGCCTGAGGTGAGGAGTTCAAGACCAACATGGCCAACATAGCGAAACCCTGTCTC
ss.AC003042	90910 90920 90930 90940 90950 90960 TACTAAAAAATAAAAAAAGTCAAGCGTGGTAGTGGGCACCTGTAATCCCAGCTACTTG
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ss.AC003042	91030 91040 91050 91060 91070 91080 CGAGCCATTGCACTCCAGCCTGGGCAACAATAGTGAAACTCTGTCTGAAAAAATAAAAAAT
ss.AC003042	91090 91100 91110 91120 91130 91140 ATGACTGGACCTTTTATTACCTTTTTTTTTTTTTTTTTTTTTTTTGGAGATGGAGCTTTAC
ss.AC003042	91150 91160 91170 91180 91190 91200 TCTTGTTGCCCAGGCTGGAGTGCAATGTGCGATCTCAGCTCACTGCAACTGCCGCCTCCC
	91210 91220 91230 91240 91250 91260

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	91270 91280 91290 91300 91310 91320
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	91330 91340 91350 91360 91370 91380
ss.AC003042	CTAGTCTTGAACCTCCTGAGCTCAGGCAATCCAAGTGCCTCGGCCTCCCAAAGTGTGGGA
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ss.AC003042	TTATAGGCGTGAGCCACCGCGCCAGTCGCTCTTCTTTTTTCTTTTGAACGGAGTCT
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ss.AC003042	CCACCATGCTCAGCTAATTTTTGTATTTTAGTAGAGATGGGGTTTCACCACGTTGGTCA
	91630 91640 91650 91660 91670 91680
ss.AC003042	GGATGGTCTCGACCTCCAGACCTCATGATCTGCCTGCCTTGGCCTCCCAAAGTGCTGGGA
	91690 91700 91710 91720 91730 91740
ss.AC003042	TTACAGGCGTGAGCCACCGCGCCCGGCCTTATTACTCTGCTGACCCCATCTTTTATTACT
	91750 91760 91770 91780 91790 91800
ss.AC003042	GTTCCCTTCATTCATCTGGCTCCAGCCACAAGGGCTTCCTTACTATTCTCAACATGCC
	91810 91820 91830 91840 91850 91860
ss.AC003042	AATAAAACCCCAACCTCAGAACCTTTACACTAGCTGTCCCTTCTCTGCCTTCCCCCAGT
	91870 91880 91890 91900 91910 91920
ss.AC003042	TTTCTACAAGATTGCTTGCTCACTTCATTCAAATCTATATTCAATGTCAATTTTATCAGG
	91930 91940 91950 91960 91970 91980
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	91990 92000 92010 92020 92030 92040
ss.AC003042	TACTGATTTTTCTAACTTATCATCCCTGACAAATTGAATATTTGCTTTCTGTCTGCCTCT
	92050 92060 92070 92080 92090 92100
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ss.AC003042	ATTAAATCAGACTCAATCTTTCCATCAAGAAAATAAGCTGCCACTGTCACCAAGCTGTTT
	92170 92180 92190 92200 92210 92220
ss.AC003042	TAAATTTTAACAAACCCATTTTCTCCTAATTGATTATACTTACCCATGTACATAAAATAA
	92230 92240 92250 92260 92270 92280
ss.AC003042	TGTATAAAGCTTCTTTGCATCAGTCATGCAGCTTCTAGTTACAGACAGGACTCCCTTG
	92290 92300 92310 92320 92330 92340
ss.AC003042	CCCTACTGTTAGGGGTTCAAGAGCAGGATTTCCAGACTCTACAAGCTGGGAAAAGAGACG
	92350 92360 92370 92380 92390 92400

ss.AC003042	CTCCACACTGCGACGACAACCAACACATGGGACAAGCTGAGAAAGTGCCTCAGGACTTC
	92410 92420 92430 92440 92450 92460
ss.AC003042	GCGTGATGTCACCACCATGGCAATACTTAGATCCTGTTGCTTAAGCATACCATGTGCGCTG
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	92530 92540 92550 92560 92570 92580
ss.AC003042	CTACTGGTTTCCTATCCTTGTGCAGTAAAGTACAACCTGGCCAGGGTTTACCAGCTCTACC
	92590 92600 92610 92620 92630 92640
ss.AC003042	TGCAACTGAGTCAGAAAGGCAAAGTAGTCAGCTTTGTCCATGCTGTACGGAATTTCTCTCC
	92650 92660 92670 92680 92690 92700
ss.AC003042	ACAAACCCCTTGCTCTAGAATCTAGGGTATATAAACAACCTCTGCTTAGGATGCCAAAAA
	92710 92720 92730 92740 92750 92760
ss.AC003042	GCAGTACTGCATCTGGAAATGTAGGGCTGGTTCAGTGAGTATTAGGCCAGTCCTCTCACA
	92770 92780 92790 92800 92810 92820
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	92830 92840 92850 92860 92870 92880
ss.AC003042	TTTGTTTTTGTTTTTTGAGACGGCATCTTGCTCTCTCGCCAGGCTGGAGTGCAGTAGCAC
	92890 92900 92910 92920 92930 92940
ss.AC003042	AATCTCAGCTCACTGCAACCTCTGCCTCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCTC
	92950 92960 92970 92980 92990 93000
ss.AC003042	CCGAGTAGCTGGGACTACAGGTGTGCACCACCACGCCCGGCTAATTTTAGTATTTTAGT
	93010 93020 93030 93040 93050 93060
ss.AC003042	AGAGATGGGGTTTCACCATGTTGGCAAGGATGGTCTTGATCTTTTGACCTTGTGATCCAC
	93070 93080 93090 93100 93110 93120
ss.AC003042	CCGCCTCAGCCTCCCAAAGTGCTCGGATTACAGGCGTGAGCCACCACGCCTGGCCTGTTT
	93130 93140 93150 93160 93170 93180
ss.AC003042	TTTTTGTTTTGTTTTGTTTTGACAACCTTTTAACAACACACTTACTATCACTATGTTTAGC
	93190 93200 93210 93220 93230 93240
ss.AC003042	TACAGGAGTCAAGTTAGGATGGTAATCATATGGAGCAGCAATTCCCAATCCAGAGGCATG
	93250 93260 93270 93280 93290 93300
ss.AC003042	AACAGGTATATTACGAATTAATGGGAGAAAACATGGCCTATCTTCCTTATGTAGGGAAGT
	93310 93320 93330 93340 93350 93360
ss.AC003042	AACTAGCATGCTGCTGCTTATGAATTGTATCTGCTGGTTATGACAAGGTAGAAAAATAAC
	93370 93380 93390 93400 93410 93420
ss.AC003042	TGAGAGCTACTGTTGCAGAGAAATGAGCAAACCTCTAGTAAGTAACCTTCTACCTGATGGAG
	93430 93440 93450 93460 93470 93480
ss.AC003042	TTATAGTTAACTGCAGTTAACTTTTCTAGATTTGCCAAAAACGGATAGGAAAGTAGGACA
	93490 93500 93510 93520 93530 93540

ss.AC003042	ATTCCCAAGAAGCATTTTCTCACATTTACCATTACCCTTCCATTCAAAGTTTTCTTAAAA
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ss.AC003042	93610 93620 93630 93640 93650 93660 AGCCCTCCATATCCATGGGTTCTACATCTGTGAATTTAACCAACCAAGGATCGAAAATAT
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ss.AC003042	93850 93860 93870 93880 93890 93900 TCTGAGACAAGGTCTCACTCTATTGCCCAGGCTGGAGTGCAGTGATGCGATCTCAGCTGA
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ss.AC003042	94090 94100 94110 94120 94130 94140 GCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCATGCCTAGCCCTTACTATATCAT
ss.AC003042	94150 94160 94170 94180 94190 94200 TTTGTATAAGCATTTGTGGATTTTGGTTTGCCTAGGGATCCTTGAACCTATCCCCACGGAT
ss.AC003042	94210 94220 94230 94240 94250 94260 ACTGAGGGACCACTATACATTGCATTTAAGTGTATTTATAAAGCACTATATTTCTCAGGA
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ss.AC003042	94330 94340 94350 94360 94370 94380 TACAGCAGAAAACCAACAAGTTTTTAATGAAAAATTATATACCTTATCTTTTAAAAACTA
ss.AC003042	94390 94400 94410 94420 94430 94440 GGAAAGATGGCCTGGTTTTAAATTAAGTCTTATGGACATGTAAATATTAACACACCA
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ss.AC003042	94510 94520 94530 94540 94550 94560 TATAGCAATGGTGAAAGAGCAATTCCAGTGCAATATTAAGACCTAGAGAATCCTATATAA
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	94630 94640 94650 94660 94670 94680

ss.AC003042	GATTGAAAAAACTATTACCTGAATGAACTGCTTTAGCTGTGCACCATTATTCTGATGTCC
ss.AC003042	<div> <div>94690</div> <div>94700</div> <div>94710</div> <div>94720</div> <div>94730</div> <div>94740</div> </div> ATCGAGATTTAACACATTATCAGGAAATTCCATCACCATCTTAAATGCAAACAGAACGG
ss.AC003042	<div> <div>94750</div> <div>94760</div> <div>94770</div> <div>94780</div> <div>94790</div> <div>94800</div> </div> AAATCAATTACTTTACCCCTCTGAGAACAGGATACAGCCTACAACTCCAGAAATAGACC
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ss.AC003042	<div> <div>94990</div> <div>95000</div> <div>95010</div> <div>95020</div> <div>95030</div> <div>95040</div> </div> CCCATCTCTACTAAATACATAAAATTAGGCAGGTTTGGTGGCGCATGCCTGTAATCCTAG
ss.AC003042	<div> <div>95050</div> <div>95060</div> <div>95070</div> <div>95080</div> <div>95090</div> <div>95100</div> </div> CTACTTGGGAGGCTGAGCCAGGAGAACCCTTGAACCCGGGAGGCAGAGGTTGCAGCGAG
ss.AC003042	<div> <div>95110</div> <div>95120</div> <div>95130</div> <div>95140</div> <div>95150</div> <div>95160</div> </div> CTGAAATCGCACCCTGCCTCCAGCCTGGACAACAAGAGTGAACTCTGTCAAAAAAAAA
ss.AC003042	<div> <div>95170</div> <div>95180</div> <div>95190</div> <div>95200</div> <div>95210</div> <div>95220</div> </div> AAAAAAAAAAAAAAAAAAAAAAAAAAATTCAGTACATAAGACAAGTTTCCATTTTTTTTTT
ss.AC003042	<div> <div>95230</div> <div>95240</div> <div>95250</div> <div>95260</div> <div>95270</div> <div>95280</div> </div> TTTTTTTTTTGAGACGGAGTCTTGCTCCGTACCTAGGCTGGAGTGCAGTGGCATGATTT
ss.AC003042	<div> <div>95290</div> <div>95300</div> <div>95310</div> <div>95320</div> <div>95330</div> <div>95340</div> </div> AAGCTCATCACAACTCCACCTCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCTCGCGAG
ss.AC003042	<div> <div>95350</div> <div>95360</div> <div>95370</div> <div>95380</div> <div>95390</div> <div>95400</div> </div> TAGCTGGGATTACAGGAACCCACCACCAAGCCCAGCTAATTTTTGTATTTTTAGTAGAGA
ss.AC003042	<div> <div>95410</div> <div>95420</div> <div>95430</div> <div>95440</div> <div>95450</div> <div>95460</div> </div> TGGGTTTTACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGCCTCCCAAAGTA
ss.AC003042	<div> <div>95470</div> <div>95480</div> <div>95490</div> <div>95500</div> <div>95510</div> <div>95520</div> </div> CTGGGATTACAGTCGTGAGCCACTGTGCCTGGCCAGAACAGTACCTGCCTGGCACATAGT
ss.AC003042	<div> <div>95530</div> <div>95540</div> <div>95550</div> <div>95560</div> <div>95570</div> <div>95580</div> </div> AAATGTTTGCTCTAATTATGAACAAAAGGGCACATTGATATACTTATTCAATTATCAAA
ss.AC003042	<div> <div>95590</div> <div>95600</div> <div>95610</div> <div>95620</div> <div>95630</div> <div>95640</div> </div> ATTCACTACCATAGGAAGGCATATGAACTTAAGGAGGCTTCACTATGTCACATAATGGG
ss.AC003042	<div> <div>95650</div> <div>95660</div> <div>95670</div> <div>95680</div> <div>95690</div> <div>95700</div> </div> AATGTGTAATTAGTACATTTTACTGATCTGTTGTACACCACAGATTTTTAGTACCATAG
ss.AC003042	<div> <div>95710</div> <div>95720</div> <div>95730</div> <div>95740</div> <div>95750</div> <div>95760</div> </div> TTATGTATCACTACAAGCCATTTTACTATAAGATGTCATCAAATTCAAGCAGCATCCTG
	<div> <div>95770</div> <div>95780</div> <div>95790</div> <div>95800</div> <div>95810</div> <div>95820</div> </div>

ss.AC003042	ATTTTCAGGTATTAAATGTGGGGGAAAAAGATATGCCTTCAAAACAATGAAAGTAACACA
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ss.AC003042	TGTATATCTTAATAAAACATTGTTAAAGATCAAACATATCGTACTAGGACAAACTATTT
	95890 95900 95910 95920 95930 95940
ss.AC003042	CCACATTGCCACATAACAAGGACCACAACTCCTACAAAATCAAAGAGTGAAGTCAAGAG
	95950 95960 95970 95980 95990 96000
ss.AC003042	AAAAACACCGATTTAAGGCAAAAACAAAATATCCCTACCCAGTTGAATGCGATCTTAAAA
	96010 96020 96030 96040 96050 96060
ss.AC003042	AGATCACTCCCTTCCCCAACCAGCACCAGAGACCTGCTTCTTTAATAGATGTAACCATTC
	96070 96080 96090 96100 96110 96120
ss.AC003042	CTTTCCTTCCATATTAGAGAAATTTAAACATGTTTGTTCTAACAGCAAAATGAGGCCTC
	96130 96140 96150 96160 96170 96180
ss.AC003042	ATTAACAGCTAAGTCAAACGTAAGCAATAGATTTAAGAGTTTTTCTTGATAACGGAGGAA
	96190 96200 96210 96220 96230 96240
ss.AC003042	TATGAGATATATGAAGTACAGAGACAAATAGATACTAAAGGATAGACTATGATGCAAATA
	96250 96260 96270 96280 96290 96300
ss.AC003042	CTAACATAATCCAGACTGCATGTGCAACACACTTCAAATTTTCAGTGTGTATACTTTATC
	96310 96320 96330 96340 96350 96360
ss.AC003042	TTTCAAAAAGGAAAACATATTAGATGTGGCTATCTCTAGGTAGTAAGACAACCTTTTTCT
	96370 96380 96390 96400 96410 96420
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	96430 96440 96450 96460 96470 96480
ss.AC003042	GGGAAGAGTTAATGCTCCTTGCTTCCAATTCTATATTCACTATAACCATGTTTAGAGACAT
	96490 96500 96510 96520 96530 96540
ss.AC003042	GCTTCCATTTCAATAGCTTTTTTTTTTTTTTTTTTTTTTTTGGAGACAGAGTCTTGTTCTGTCAC
	96550 96560 96570 96580 96590 96600
ss.AC003042	CCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTGCAACCTCCGCCTCCCAGGTTCAA
	96610 96620 96630 96640 96650 96660
ss.AC003042	CCAATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCTGCCACCAAACAT
	96670 96680 96690 96700 96710 96720
ss.AC003042	GGTTAATATTTTGTATTTTATAGTAGAAACAGGGTTTTGCCATGTTGCCAGGCTGGTTTC
	96730 96740 96750 96760 96770 96780
ss.AC003042	AAACTCCGGAGCTCAGGCAATCTGCCTGCCTCGGACTCCCAAAGTGCTGGGATTACAGGC
	96790 96800 96810 96820 96830 96840
ss.AC003042	GTGAGTCACCACGCCTGACCCATTTCAATAGCTTTTACCATTCTGAAAGTTTTTCTTCC
	96850 96860 96870 96880 96890 96900
ss.AC003042	ATGCATACAGATGAAATGTCCAAATGTCAATTATCCAATTTTCAGGTTTATCAACCCTGA
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ss.AC003042	CATCTTGTTTCTAGTTTTCTTCTCAGTCTTATTAATACCTCTAAAGGGGGGTAGCAATA
ss.AC003042	<div>96970 96980 96990 97000 97010 97020</div> AGTAATAATAAAGACACTTCATGTGTATTAGACATTGTTATAAGCACTTTCATACATTAA
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ss.AC003042	99310 99320 99330 99340 99350 99360 TGGCCGGGCGCATTGGCTCACGCCTGTAATCCCACCACTTTGGGAGGCCGAGGCAGGCAG
ss.AC003042	99370 99380 99390 99400 99410 99420 ATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAAAATGGTGACGCCTCGTCTCTAC
ss.AC003042	99430 99440 99450 99460 99470 99480 TAAAAATACAAAACCTAGCCGGGCATGGTGGCGGGCGCCTGTAATCCCAGCTACTCAGGA
ss.AC003042	99490 99500 99510 99520 99530 99540 GGTTGAGGCCCAAGAATCACCTGAACCTGGAAGGCGGAGGTTGCAGTGAGCCAAGATCAC
ss.AC003042	99550 99560 99570 99580 99590 99600 ACCACTGCACTCCAGCCTAGGTGACACAGTGAGACTCCATCTCGAAAAAAAAAAAAAGAA
ss.AC003042	99610 99620 99630 99640 99650 99660 ATATCATAGCAATCTGACAATATGTACCTGGAACCTTACAAAAGTTCTTATCCTTTGAT
ss.AC003042	99670 99680 99690 99700 99710 99720 CCAACCAGTAATTCCACTTCCAAAAGCCTGAGAAAACATTTTAATGCAAAGATTTTGTCA
ss.AC003042	99730 99740 99750 99760 99770 99780 TTATTTATGTTCTTACAGTTTATTCATAGCAAAAACCTAGAACACCTCCATGTCCAACAG
ss.AC003042	99790 99800 99810 99820 99830 99840 TGGAAAAATAATTACAGAAATGTCATACAACGGAATATTACACAGCCATTAAAAATGTTTA
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ss.AC003042	99910 99920 99930 99940 99950 99960 TTACAGAAATATATTAACCTGTATCTGTGTGTCTAGGACTGAAATTACACCAAATGTGCTTA
ss.AC003042	99970 99980 99990 100000 100010 100020 TCCCTGAGAAGCATGACTAAGGGTAATTTGTTTTGTAGTTATTTTTCAAGATTTTAGAAG
ss.AC003042	100030 100040 100050 100060 100070 100080 GAATATATATTTTGGCCGGGTGTGGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGC
ss.AC003042	100090 100100 100110 100120 100130 100140 CGAGGCGGACAGATGACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATAGGGAAA
ss.AC003042	100150 100160 100170 100180 100190 100200 CCCCCATCTCTTCTAAAAATACAAAAAAATTAGCTGGGCGTGGTGACACGCACCTTGTAAT
ss.AC003042	100210 100220 100230 100240 100250 100260 CCCAGCTACTCAGGAGGCTGAGGCAGGAGAATCACTTGAGCCTGAGAGGCAGAGGTTGCA
ss.AC003042	100270 100280 100290 100300 100310 100320 GTGAGCCAAGATCAGGCCACTGTACTCCAGCCTGGGCGACAGAGCGAGACTGTGTCTCAA
	100330 100340 100350 100360 100370 100380

ss.AC003042	AAAAAAAAAACTTTAATTCTTCAGATTTCTCTAAAATCAAATATGTATTCTATCTGTTA
ss.AC003042	100390 100400 100410 100420 100430 100440 TTTTATAATTGTAGTAACACTGAACAACATTTTAGCCAGAGTATAAACTTTCTTAAATA
ss.AC003042	100450 100460 100470 100480 100490 100500 TTTACCATTCCACCAACTTATTTGGAATTTTCTCAAGTACACCTACATCAGCCCTATCC
ss.AC003042	100510 100520 100530 100540 100550 100560 TATACTCAGGTGTTCAAACCTCACTGAACCTACCATGGGAATCTTCTAAACATGGACACAAC
ss.AC003042	100570 100580 100590 100600 100610 100620 ATATCACATAAAAGAAGAGGCTATTTTTTTTTTTTGAACGGAGTTTCACTTTGTCTCCCA
ss.AC003042	100630 100640 100650 100660 100670 100680 GGCTGGAGTGCAGTGGCGCAATCTTGGCTCACTGCAACCTCCGCCTCTGGGGGTTCAATC
ss.AC003042	100690 100700 100710 100720 100730 100740 AATTCTCTTGCCCTCAGTCTCATCAGTAGCTGGGTCTACAGGCACACTCTACCACACCCAC
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ss.AC003042	100810 100820 100830 100840 100850 100860 CTCCTGAGCTCAGGCAATCTGCCAGCCTCGGCCTCCCAAAGTGCTAGGATTACAGGCATG
ss.AC003042	100870 100880 100890 100900 100910 100920 AGCCACAGCACCGGGCCTAAGGCTACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
ss.AC003042	100930 100940 100950 100960 100970 100980 TTTTTTTTTTTGAGACAGAGTCTTGCTCTTGTTGCCCAGGCTGGAGTGCAGTGGTGCAT
ss.AC003042	100990 101000 101010 101020 101030 101040 CTCGGCTCACCGCAACCTCCACCTCCCGGTTTCATAGGATTCTCCTGCCTCAGCCTCCTG
ss.AC003042	101050 101060 101070 101080 101090 101100 AGTAGCTGGGATTACAGGCACCCACCTATGTCTGGCTAATTTTTGTATTTTTAGTAGA
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ss.AC003042	101230 101240 101250 101260 101270 101280 TACTTCTTTACATACAAGTTTGTTAATTTTCAATTTTACAAGTCCAAATTACAACCTGCCAGT
ss.AC003042	101290 101300 101310 101320 101330 101340 TTAACTAAGGGTAAAGTTTCAGCATCCCAAATAAAATGATAAAGTCTGCAACTGCCTGTA
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ss.AC003042	101410 101420 101430 101440 101450 101460 ATAAGTTCAAACAATGTTTCCTCAGTGCATTACCTACAGACCCTAGGGACAAAGACAAA
	101470 101480 101490 101500 101510 101520

ss.AC003042	CCTAAGGTAACTTCAGGCATCCACTGCCATCTATCAAAGGAACAATGCAGAGCATAAAA
ss.AC003042	101530 101540 101550 101560 101570 101580 CTCTGATAGGGGCATCTTCCTTCCCTCTTCCCTTTTCCCCTTCTCTCCCAACAGGTGTTT
ss.AC003042	101590 101600 101610 101620 101630 101640 TGCTCTGCATTCTCCCTTTCAGTAGTATTTGGTAGAATATCCTGAAAGAACTTGTTTCC
ss.AC003042	101650 101660 101670 101680 101690 101700 CTTGACAAGAATTTTCTACTAACATTCACTCACAGCATTCAATGACTGTGCAGAAGTCCCA
ss.AC003042	101710 101720 101730 101740 101750 101760 GCACAAATAAATGTCTCACTCATTCCTTTGTGATAAAAACCCATTCTGAAGCAAAGAAAA
ss.AC003042	101770 101780 101790 101800 101810 101820 ACTGCACCTTTTCTAAATGTTATTTTGAGATATTTAAATTAAGTGAGCTTAAGTTTTAT
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ss.AC003042	101890 101900 101910 101920 101930 101940 AAAGTAAGTTCCATACTAAACCACATTGCAAGGTTACATCTTTTTCAGTGAAAATTTTG
ss.AC003042	101950 101960 101970 101980 101990 102000 GAAAGTCACATCATTGTGGAGAGAATACAGTATAAAAGCACTTAAAAAGTTGGCCATTTT
ss.AC003042	102010 102020 102030 102040 102050 102060 AAAGTGCTATATGACAGATGTATTAATGTGCTGCATTACAAAGGTGGTTATGTGAATAT
ss.AC003042	102070 102080 102090 102100 102110 102120 ACCAAGAACTAGTGTCTTTTGAAGACTATTTATGTTGGTTTTCCCTATGTTTTGATATGT
ss.AC003042	102130 102140 102150 102160 102170 102180 TTTCCTATGTTATGATTATTCATTAAATAATAATCTTATATCCAAACTCACTGAATTTTT
ss.AC003042	102190 102200 102210 102220 102230 102240 TTTTTTAACTCCACAGCCATTGTGGGACAATAAACCTTAAAGGCTGATATCATAACTATA
ss.AC003042	102250 102260 102270 102280 102290 102300 TGCTTCAGAAAAGTGTTTATGTTAGCAGGGGAGAGAAGAAAGAAATATCAACAAATGAA
ss.AC003042	102310 102320 102330 102340 102350 102360 TCCCTATCTGAAGTCCAAACTGAGAAATGCATTATTTAATATGATCACAGTGCTAGTTTC
ss.AC003042	102370 102380 102390 102400 102410 102420 AACTATTTAAAAATACAAGTCCATTATACTTCTAATGCAAAAAGTACAGAAATCATAATC
ss.AC003042	102430 102440 102450 102460 102470 102480 AAGACACACAATTTCTAATGCATCAACACTATTTACTTTTATGTCAGAACAAATCATTCTA
ss.AC003042	102490 102500 102510 102520 102530 102540 CCTTTTTTCATGAAAAATAAATGCACTTGAATAATTAGAAATGCTGTCACTTAAAACTT
ss.AC003042	102550 102560 102570 102580 102590 102600 CTAATAAATTAAGTCATTCAATAGCTCTTCTAATCCTTTTTTAAAGTACTGCAGCTCAATC
	102610 102620 102630 102640 102650 102660

ss.AC003042 AAGTCTTAATTGAGACTGGCAAGCATAAAGGCATAGACTGGCATCTCTACAATGACTTGC

102670 102680 102690 102700 102710 102720
ss.AC003042 ATTTTACATAAAATTTGAAAAAAGCTTCGGTAGATATTTGCAAAAAAATATTGAGGAAC

102730 102740 102750 102760 102770 102780
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102790 102800 102810
ss.AC003042 CACCTTATCGAAATAAGCAAATGTATAATCCAAAGCTT

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